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OM nucleic - nucleic search, using sw model

Run on: July 31, 2004, 00:43:11 ; Search time 199.085 Seconds

(without alignments)  
7852.389 Million cell updates/sec

Title: US-09-963-521-1

Perfect score: 2817  
Sequence: 1 aatgaataatccccccacc.....tgatctgtccgcagctgc 2817

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 segs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents NA: \*  
1: /cgn2\_6/prodata/2/ina/5A COMB.seq: \*  
2: /cgn2\_6/prodata/2/ina/5B COMB.seq: \*  
3: /cgn2\_6/prodata/2/ina/6A COMB.seq: \*  
4: /cgn2\_6/prodata/2/ina/6B COMB.seq: \*  
5: /cgn2\_6/prodata/2/ina/PCTUS COMB.seq: \*  
6: /cgn2\_6/prodata/2/ina/backfilseq1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2817	100.0	2817	4 US-09-431-099-1	Sequence 1, Appli
2	1836.6	65.2	1909	4 US-09-431-099-3	Sequence 3, Appli
3	157.8	5.6	4403765	3 US-09-103-840A-2	Sequence 2, Appli
4	157.8	5.6	4411529	3 US-09-103-840A-1	Sequence 1, Appli
5	149.4	5.3	36138	4 US-08-311-731A-136	Sequence 136, App
6	72.2	2.6	536165	4 US-09-214-808-1	Sequence 1, Appli
7	71.6	2.5	1446	2 US-08-569-150A-2	Sequence 1, Appli
8	71.6	2.5	2868	4 US-08-274-121B-1	Sequence 2, Appli
9	70.2	2.5	1479	4 US-09-489-039A-7037	Sequence 7037, Ap
10	56	2.0	1455	4 US-09-328-352-595	Sequence 595, App
11	48	1.7	654	4 US-09-651-163A-36	Sequence 36, Appli
12	47.6	1.7	7218	4 US-08-232-463-14	Sequence 14, Appli
13	45.8	1.6	381	4 US-09-198-452A-1	Sequence 4023, Ap
14	45.6	1.6	381	4 US-08-956-171E-4023	Sequence 4234, Ap
15	44.8	1.6	400	4 US-08-956-171E-4234	Sequence 4, App
16	44.8	1.6	3000	1 US-07-841-997A-3	Sequence 3, Appli
17	44.8	1.6	3000	1 US-08-290-301-3	Sequence 3, Appli
18	44.8	1.6	3000	1 US-09-013-598-3	Sequence 3, Appli
19	44.8	1.6	5981	4 US-08-290-301-83	Sequence 83, Appli
20	44.8	1.6	5981	4 US-09-013-598-83	Sequence 83, Appli
21	44.6	1.6	4403765	3 US-09-103-840A-2	Sequence 2, Appli
22	44.6	1.6	4411529	3 US-09-103-840A-1	Sequence 1, Appli
23	44.4	1.6	237	4 US-08-956-171E-4566	Sequence 4566, Ap
24	44.4	1.6	239	4 US-08-956-171E-4543	Sequence 4543, Ap
25	44.4	1.6	239	4 US-08-956-171E-4544	Sequence 4544, Ap
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34	43.4	1.5	1171	4 US-08-956-171E-3539	Sequence 3539, Ap
35	42	1.5	339	4 US-08-956-171E-4263	Sequence 4263, Ap
36	41.2	1.5	400	4 US-08-956-171E-4029	Sequence 4029, Ap
37	41.2	1.5	536165	4 US-09-214-808-1	Sequence 1, Appli
38	39.2	1.4	399	4 US-09-621-976-8976	Sequence 8976, Ap
39	38.8	1.4	59	4 US-08-956-171E-4959	Sequence 4959, Ap
40	38	1.3	150	2 US-07-829-461A-8	Sequence 8, Appli
41	38	1.3	390	4 US-09-197-649-7	Sequence 7, Appli
42	37.4	1.3	234	4 US-09-489-039A-6372	Sequence 6372, Ap
43	37.4	1.3	303	4 US-09-489-039A-5694	Sequence 5694, Ap
44	37.4	1.3	6091	4 US-09-453-702B-200	Sequence 200, App
45	37.2	1.3	114	4 US-08-956-171E-4803	Sequence 4803, Ap

## ALIGNMENTS

RESULT 1									
US-09-431-099-1									
Sequence 1, Application US/09431099									
Patent No. 6410705									
GENERAL INFORMATION:									
APPLICANT: Degussa-Höls AG									
TITLE OF INVENTION: Forschungszentrum-Joachim GmbH									
FILE REFERENCE: New nucleotide sequences coding for the three gene and process for									
CURRENT FILING DATE: 1999-11-01									
NUMBER OF SEQ ID NOS: 4									
SOFTWARE: PatentIn Ver. 2.1									
SEQ ID NO 1									
LENGTH: 2817									
TYPE: DNA									
ORGANISM: Corynebacterium glutamicum ATCC14752									
FEATURE:									
NAME/KEY: CDS									
LOCATION: (398)..(1864)									
OTHER INFORMATION: thrE-Gen									
US-09-431-099-1									
Query Match									
Best Local Similarity 100.0%; Score 2817; DB 4; Length 2817;									
Matches 2817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	1	AATGAATATATCCCTCAACCACTGGGCAATTCGAACCGGTTTCATTTCGAACATCG	60						
QY	61	AGCCAGGGAAGAAAGAGCCCTTAAGCCCGGTTATTAAGGAGACTTGGAGACC	120						
DB	61	AGCCAGGGAAGAAAGAGCCCTTAAGCCCGGTTATTAAGGAGACTTGGAGACC	120						
QY	121	TCAACCCAAAAGGGGCAATTCATTAAAGAAATACCCCTTGACCTGGTGTATTGAGC	180						
DB	121	TCAACCCAAAAGGGGCAATTCATTAAAGAAATACCCCTTGACCTGGTGTATTGAGC	180						
QY	181	TGAGAGAGAGCTTGAACCTCAACCTGAGCTTCAAGTGGTGGCGTGGCAATTCGG	240						
DB	181	TGAGAGAGAGCTTGAACCTCAACCTGAGCTTCAAGTGGTGGCGTGGCAATTCGG	240						
QY	241	CCACTCCAGCACCGGAGATGCTGATCAACCAATGAGATACATCTTATGCTATGT	300						
DB	241	CCACTCCAGCACCGGAGATGCTGATCAACCAATGAGATACATCTTATGCTATGT	300						
QY	301	GTAATGCAATGGAATTCGGGGCTAAGATATCTGTGAACCGGTGATTAACGACCTGTG	360						
DB	301	GTAATGCAATGGAATTCGGGGCTAAGATATCTGTGAACCGGTGATTAACGACCTGTG	360						

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 Db 361 ATTGAGCTGTTTTCTGTGCAAAATGTTTTCAAGCAATGTGATTTTGCGACCCCTTG 420  
 QY 421 TGGCGCATTTCAACAGTTGAGCGTGCAGAAAGCCGCACTCCGCACTGCACTAGCCCC 480  
 Db 421 TGGCGCATTTCAACAGTTGAGCGTGCAGAAAGCCGCACTCCGCACTGCACTAGCCCC 480  
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 QY 541 CGATATTTGCTTTCTTCAGATAGTCAAGTCAACAGTATACCAAGGTGCAAGTTGAGCGGT 600  
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 QY 601 GACCTCTGCGTATGCGCTGTATCTATAGCATGTGATATACGTTGATATGATACACAT 660  
 Db 601 GACCTCTGCGTATGCGCTGTATCTATAGCATGTGATATACGTTGATATGATACACAT 660  
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 Db 721 GTTGACACCAACTCTTCACAACTGTGAGGTTGACCGTTGATCCGTTCAATTCAGGC 780  
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 Db 781 TGTGTCTACCCGCTGAGGTTGCGGAGAAATTTGAGACGATGTGAGCAATGCGCTGC 840  
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 Db 841 GTCTTATGCTTCCCTGTGTGAGGTTGCTGCGGCAATGATGAGTGGCGCTGTGCTGT 900  
 QY 901 GCTGTGAGTGTGATGAGGATTTCCCTAATGTCTTTATTAACCGGTTGACATCAT 960  
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 Db 1141 ACTTGTGCAATCTTCTGAGAGAGGATCAACGCGGCTCCGCTGAGCAAGTCAAGAT 1200  
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 Db 1261 TTTTGAACACTCGGTTTACCGCGGCAATTTGCTGTGCGTGTGCGGATTCAGCT 1320  
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 Db 1381 TTAACGCGAGTGTCTCGGTGATTTATGCGGCGCTTACGCGCTGATGAGTTCTCGCT 1440

QY 1441 TTAATACCTTCGTTGTTTATTTAGAGCCCGCTCTGCGGCTGCGATTGCTCAACAGC 1500  
 Db 1441 TTAATACCTTCGTTGTTTATTTAGAGCCCGCTCTCTGCGGCTGCGATTGCTCAACAGC 1500  
 QY 1501 AGTTGGTTTCACTGATGTTGCTTCCCGCTGATTTCTGATTCACCGTTGATTTGGC 1560  
 Db 1501 AGTTGGTTTCACTGATGTTGCTTCCCGCTGATTTCTGATTCACCGTTGATTTGGC 1560  
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 Db 1621 CTTGAATGATCAAACTCATGAGTTTCAACCAATTTCCGTTGCTTTTACCACTGCTTC 1680  
 QY 1681 ATCACTTCCGCTGCGCTGTTTGGTGTGATGATTTGCTGAGGATGCTGCTGCTCAC 1740  
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 Db 1801 TGACAGATATGAGCGCGAGAGAGAAAGCTCAAGACTAATCAAGATTGCTAATTA 1860  
 QY 1861 AAGTAAATATCAACCTGTGATGAGGCTTTCGCTTAAATGCGTGAATTTGGGCTGA 1920  
 Db 1861 AAGTAAATATCAACCTGTGATGAGGCTTTCGCTTAAATGCGTGAATTTGGGCTGA 1920  
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 Db 1921 TCGCTTTTAAACATCGAGAGGATCCTTTCGCGGCAAAATGACGAGACCTGCTCCACC 1980  
 QY 1981 CAGATCCCTTCAAGCTGTGTGAAGAGAAACCGAGCGGCTGCGGAGATTTGTTGCA 2040  
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 Db 2101 AGGCTGCGTTAACAAGAGGCTTCTGAACAGAGAAAGCTGAGCAAGAGCTA 2160  
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Db 2521 CTGCAAGTGAATGAAGGCTTCTACGAGGCTTTTCAACGCAACGCTGTGCTCTTT 2580  
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Db 2581 TTCCAGATTTGATTTTACTCTCCGATGTACCAACCGATTTGGTGGCATCGTTTGGGGAAG 2640  
QY 2641 TAAACCTAAGTTGCTTAAAGCCGTGAGCCCAAGTGGCGGCAACGCTGCCACTGTGTGGG 2700  
Db 2641 TAAACCTAAGTTGCTTAAAGCCGTGAGCCCAAGTGGCGGCAACGCTGCCACTGTGTGGG 2700  
QY 2701 TGCAGGATATCAGCTGTGTGTGTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2760  
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Db 2761 AGATCGGTTTCTCTCCACATTCGCTTCCCTCCCGGATCTGTGCTGTGCTGTGCTGTG 2817

RESULT 2  
US-09-431-099-3  
Sequence 3, Application US/09431099  
Patent No. 6410705  
GENERAL INFORMATION:  
APPLICANT: Degussa-Höls AG  
APPLICANT: Forschungszentrum-Jülich GmbH  
TITLE OF INVENTION: New nucleotide sequences coding for the thrE gene and process for  
FILE REFERENCE: 990079 BT  
CURRENT APPLICATION NUMBER: US/09/431,099  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 3  
LENGTH: 1909  
TYPE: DNA  
ORGANISM: Corynebacterium glutamicum ATCC13032  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (280) ..(1746)  
OTHER INFORMATION: thrE-Gen  
US-09-431-099-3

Query Match 65.2%; Score 1836.6; DB 4; Length 1909;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 156 CCCCTTTGACCTGTGTATTTAGCTGGAGAGAGACTTGAACCTTCAACCTAAGCATTA 215  
Db 38 CCCCTTTGACCTGTGTATTTAGCTGGAGAGAGACTTGAACCTTCAACCTAAGCATTA 97  
QY 216 CAAGTGGTGGCTGCAATTTGGCCACATCCAGCAACCGGAGAGTGTGATGATCAACAC 275  
Db 98 CAAGTGGTGGCTGCAATTTGGCCACATCCAGCAACCGGAGAGTGTGATGATCAACAC 157  
QY 276 TACGAATACGATCTTACGATATGTATCATCAACATGAAATCGGGGCTAGATATCTG 335  
Db 158 TACGAATACGATCTTACGATATGTATCATCAACATGAAATCGGGGCTAGATATCTG 217  
QY 336 GTGAACCGTGCAATAACGACCTGTGATTTGACTTTTCTTTCGAAATGTTTCCAGC 395  
Db 218 GTGAACCGTGCAATAACGACCTGTGATTTGACTTTTCTTTCGAAATGTTTCCAGC 277  
QY 396 GGATGTTGAGTTTGGAGCCCTTGTGGCGCATTTCAACAGTGAACGCGGCAAGGCGG 455  
Db 278 GGATGTTGAGTTTGGAGCCCTTGTGGCGCATTTCAACAGTGAACGCGGCAAGGCGG 337  
QY 456 CACCTCGGCATCGCACTAGCCCGGATTTGATCTCACTAGCAATGATCAAGTGGCGGCG 515  
Db 338 CACCTCGGCATCGCACTAGCCCGGATTTGATCTCACTAGCAATGATCAAGTGGCGGCG 397

QY 516 TGATGAATTTGGCTGCGAAGATTGGCGATATTTTGTCTTCTACAGTACGTCAACAGTGG 575  
Db 398 TGATGAATTTGGCTGCGAAGATTGGCGATATTTTGTCTTCTACAGTACGTCAACAGTGG 457  
QY 576 ATACCAAGTGAAGTTGAGCGGTGACCTGTGCGATATGAGCTGTACTATAAGCATGTGG 635  
Db 458 ACACCAAGTGAAGTTGAGCGGTGACCTGTGCGATATGAGCTGTACTATAAGCATGTGG 517  
QY 636 ATATCAGTGAATACGATACCAATCTTACCAACATGCTGTGTGAGAGAGATGCGCG 695  
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QY 696 TCAACGTTTTCATGTTGTGGGCAAGTTGACACCAACTTCTCCAACTGTGAGGTTG 755  
Db 578 TCAACGTTTTCATGTTGTGAGCAAGTTGAGACCAACTTCTCCAACTGTGAGGTTG 637  
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Db 698 TGACAGATTTGGAGCAATCCGCTGCTTATAGTTTCCCTGTGCTGTGCTGTGCTGTG 757  
QY 876 CAATGATGAGTGGCTG 935  
Db 758 CAATGATGAGTGGCTG 817  
QY 936 CTTTATTTACCGGTTTACGATATTCACAGAGTCAATTTTGGGAAAGAGGTTTGC 995  
Db 818 CTTTATTTACCGGTTTACGATATTCACAGAGTCAATTTTGGGAAAGAGGTTTGC 877  
QY 996 CTACTTTCTCCAAATGTTG 1055  
Db 878 CTACTTTCTCCAAATGTTG 937  
QY 1056 ATTCTTGGCGTTGCAATTTGTCTTGAATCAACCGGACCGGATGATGATCGATCGAA 1115  
Db 938 ATTCTTGGCGTTGCAATTTGTCTTGAATCAACCGGACCGGATGATGATCGATCGAA 997  
QY 1116 TTG 1175  
Db 998 TTG 1057  
QY 1176 CTCGGGTGACAGAAATGACGATTTTGTGAACATCTCTGTTTACCGGCGCATTTGTG 1235  
Db 1058 CTCGGGTGACAGAAATGACGATTTTGTGAACATCTCTGTTTACCGGCGCATTTGTG 1117  
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Db 1118 CTGGCGTGGGTTTGGCATTCAGCTTGTGAATCTTGTGATGATGATGATGATGATG 1177  
QY 1296 AGTCCGCTGACGACCTAATTTATGCTTACATTTGCGCCGATTAATGCTGTGAGGCTCA 1355  
Db 1178 AGTCCGCTGACGACCTAATTTATGCTTACATTTGCGCCGATTAATGCTGTGAGGCTCA 1237  
QY 1356 CCGCAGCGGCTTGGAGTGGGTTTACCGGAGAGTCTCGGATATTTAGCGGAGC 1415  
Db 1238 CCGCAGCGGCTTGGAGTGGGTTTACCGGAGAGTCTCGGATATTTAGCGGAGC 1297  
QY 1416 TTACTGCGGTATGAGGTTCTGCGTTTATTAACCTCTCTGTTTATTAAGCCCGTCT 1475  
Db 1298 TTACTGCGGTATGAGGTTCTGCGTTTATTAACCTCTCTGTTTATTAAGCCCGTCT 1357  
QY 1476 CTGGCGTGGGATGCTGTGCAACGAGTGTGTTTCACTGTGTGTGTGTGTGTGTGTG 1535  
Db 1358 CTGGCGTGGGATGCTGTGCAACGAGTGTGTTTCACTGTGTGTGTGTGTGTGTGTG 1417  
QY 1536 TCTGATTTCAACGTTGATTTGGGATTTGGCGGATTCACCAATGCTTCAAGTCTAG 1595  
Db 1418 TCTGATTTCAACGTTGATTTGGGATTTGGCGGATTCACCAATGCTTCAAGTCTAG 1477  
QY 1596 CAATTTACCGGAAATGTAAGCCACCTTGAATGATCAACACTCATGAGGTTTCAACACA 1655

Db	1478	CAATTACCGCGGAATGACGCCACCTCGAATGATCAAACCTCATGGCTTACCCACACA	1537
Qy	1656	TTACGGTGTGTTTAAAGCACATGCTTCATCACTTGGCCGTGGCTGGTTTGGTGAATGGA	1715
Db	1538	TTGCGGTTGCTTTAAAGCACTGCTTCATCACTTGGCCGTGGCGTGGTGGTTTGGTGAATGGA	1597
Qy	1716	TTGCGCGGAGGCTTAAGTGTGTCCACACAGCTTCAACCCATACCGTGCACTTTAACAAAGGCGA	1775
Db	1598	TTGCGCCGACGCTTAAGTGTGTCCACACAGCTTCAACCCATACCGTGCACTTTAACAAAGGCGA	1657
Qy	1776	ATGAGTTCCTCTTCCAGAGGAAAGCTGAGCAAGATCAGCGCGCGCAGAGAAAAGTCCAA	1835
Db	1658	ATGAGTTCCTCTTCCAGAGGAAAGCTGAGCAAGATCAGCGCGCGCAGAGAAAAGTCCAA	1717
Qy	1836	AGACTATCAAGAATTCGTTAATAAAGTAAAGTAAATCAACTGTCTTAAGCGCTCTTTGCT	1895
Db	1718	AGACTATCAAGAATTCGTTAATAAAGTAAAGTAAATCAACTGTCTTAAGCGCTCTTTGCT	1777
Qy	1896	TAAATAGCGTAAGAAATATCGGGTCGATCGCTTTAAACACTCAGAGAGATCTCTTCGCGGCC	1955
Db	1778	TAAATAGCGTAAGAAATATCGGGTCGATCGCTTTAAACACTCAGAGAGATCTCTTCGCGGCC	1837
Qy	1956	AAATATCAGGACATCTGTCCTCAACCCAGAAATCCCTTCAACGGTGTGTTGAAGAGAAACGGCA	2015
Db	1838	AAATATCAGGACATCTGTCCTCAACCCAGAAATCCCTTCAACGGTGTGTTGAAGAGAAACGGCA	1897
Qy	2016	GCCGGTG 2022	
Db	1898	GCCGGGG 1904	

```

RESULT 3
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match          5.6%; Score 157.8; DB 3; Length 4403765;
Best Local Similarity 58.2%; Pred. No. 1.8e-38;
Matches 310; Conservative 0; Mismatches 202; Indels 21; Gaps 1;

QY      2306   CTGTGTAATTGTTTGCTAACCGTCTGCCAGTAGATATGACTGTTCACCCCAAGTGTACTTA 2365
           ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       3902073  CTCTGTGGTGTAGGCATTCGACCTGCCGTGATCTGGAGCGCTTCTCCGACGGCAGCAC 3902132

QY      2366   TAGCATCTCCCCCAGCCCCCGGTGGCTTGTACCGGGGCTTTTCCCCTTCTGGAAACA 2425
           ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       3902133  AACCTGAAAGCAGACGCCCCCGGAGGCTTGTCACCGCCCTTGAGAGCCGGTGTGCGGGCTCG 3902192

QY      2436   TCGTGTGAGTGTGGGTGCGATGSGCCCTGGAACTGTGATTTGACCACCCGACACTTTTGAAC 2485
           ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       3902193  GGCGGGGCTCTGGGGTGGCTGGCCCTGGCGGCTTTAACGACGACGGGGGCGAACCCGACCTTCCA 3902252

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QY	2486	AGATACGGGTG-----TTTGGCAGACCCGTTGCTCACTGG	2524
Db	3902253	CGTGTGGAGCGGCCCATCATCCAGACGAGCTGGAACTTCACTCCGGTAAGGCTTGAGCAC	3902312
QY	2525	AAGTGACTATGAAAGGCTTCTACAGAGGAGCTTTTCAAAAGCAACGCTGTAGGCTCTTTTCCA	2584
Db	3902313	CACGAGACATAGCTCACTACTACAGAGGAACTTCTCCAAAGCCACACTGTGGGCGCGTTGACCA	3902372
QY	2585	CGATTTGATTGTTACTCCGGTGTACAAACCGATGTGTGCATGCGTTTCGGGAAGTAAA	2644
Db	3902373	CGAAGTCATGTCAAGCCGCTTACCAACGCGCAATGGTGGAGTGCCTACGTCGACGCTCAA	3902432
QY	2645	CTTCAAAGTTCGCTGAAGCCGTGAGCCAAAGTGCGGGACACAGGTGACACTGTGTGGGGTGA	2704
Db	3902433	CCAGCGCTTTGCGAGAGCCCGCGTCCGCGCCGCCCAAGGCGCAACCGTGTGGGTACA	3902492
QY	2705	GGAAGTACAGACTGTGTGGTGTCTCGGCATTTTGGCGCAAGATCGGCCCTGATTTGAAGAT	2764
Db	3902493	GGACTTACACACTGAGGTGTGTATCCGAAGATGCTGGCGCATGCTGGGCCGATCTGACCAT	3902552
QY	2765	CGGTTTCTTCCCTCCACATCCCTTCCCTTCCCTGATCTGTTCGGTCAAGCTGC	2817
Db	3902553	CGGTTTCTTTTGGACATCCCGCTTCCCGCGGTAAGAGCTTTTATGACAGATGC	3902605

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1      RESULT 4
2      US-09-103-840A-1
3      / Sequence 1, Application US/09103840A
4      / Patent No. 6294328
5      / GENERAL INFORMATION:
6      / APPLICANT: FLEISCHMAN, Robert D.
7      / APPLICANT: WHITE, Owen R.
8      / APPLICANT: FRASER, Claire M.
9      / APPLICANT: VENTER, John C.
10     / TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
11     / TITLE OF INVENTION: TUBERCULOSIS
12     / FILE REFERENCE: 24366-20007.00
13     / CURRENT APPLICATION NUMBER: US/09/103,840A
14     / CURRENT FILING DATE: 1998-06-24
15     / NUMBER OF SEQ ID NOS: 2
16     / SOFTWARE: PatentIn Ver. 2.1
17     / SEQ ID NO 1
18     / LENGTH: 4411529
19     / TYPE: DNA
20     / ORGANISM: Mycobacterium tuberculosis
21     / OTHER INFORMATION: H37Rv
22     / US-09-103-840A-1

```

Query Match	5.6%;	Score 157.8;	DB 3;	Length 4411529;
Best Local Similarity	58.2%;	Pred. No.1-be-38;		
Matches 310;	Conservative	0;	Mismatches 202;	Indels 21; Gaps 1;
QY 2306	CTTTGATGTTTCTCTAACCGCTGCACGATGATATACTGTCCACCCAGATGGTAGCTA	2365		
Db 3908294	CTTGCTGTGTGTAGCCATGCACTGCCCCGTCGATCTGTGAAGGTCTTCCGACCGGACGAC	3908353		
QY 2366	TAGCATCTCCCCACGCCCCCGGTGGCCCTTGTACCGGGCCCTTCCCGCTTCGTGAACACAC	2425		
Db 3908354	AACCTGGAAAACGACGCCGCCCGGAGGCTTGTGTACACCGCTTGGAGCCGGTGTGTCGGGCGCTCG	3908413		
QY 2426	TCGTGATCTTTGGGTCGTGATGGCTGTGAACCTGTGATGTTGGCAACCGGAACATTTGGAAC	2485		
Db 3908414	GCGCGCGGGCCCTGGGTCGGCTGGCCCCGGGTTAAACGACGAGGGGCCAACCCGACCTTCCA	3908473		
QY 2486	AGATACGGGCTG-----TTTGTGTGACCCCTGTTGCTCACTGC	2524		
Db 3908474	CGTGCTGACGCGCCCATCATCCAAAGACGAGCTGAACTTCATCTCCGCTGAGCGAC	3908533		
QY 2525	AAGTACTATGAAGGCTTCTACGAGGGCTTTTCAACGCAACGCTGTGGCTCTTTTCCA	2584		
Db 3908534	CACGACACTAGCTCACTGACTCTACGAGGATTTCTCCAAAGCCACACTGTGTGGCCGCTGTACCA	3908593		





QY	2697	1GGGTGCAGACATACAGTGTGGTGGTCTGGATTTGGCCAGATGGCCCTGAT	2756
Db	317578	TGGGTGCAGACTACCCCTGGATTCTCTCGCCGCGAACTGGTACAGAGGCGCTGGAG	317637
QY	2757	TTGAAGATCGGTTCTTCTCTCCACATTCCTTCCTTCCCTGATCTGTCCCTCAGCTG	2816
Db	317638	AACCGCATCGGCTTCTTCTCCACATTTCCCTGGCGCGCTGCAGAGCTACTCTTCAGATG	317697
QY	2817	C 2817	
Db	317698	C 317698	

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	Matches	222;	Conservative	0;	Mismatches	224;	Indels	6;	Gaps	1
QY	2372	CTCCCCAGCCCGCGTGGCTTGTATCAGGGGCTTTCCCGCTCTGGAACAACATCGTGG	2431							
Db	75	CGCCGCGATGCGCGGTGGCCCTTGGCCGTGGCAATACGGGGGCACTGAACCCCGAGCGG	134							
QY	2432	ATGTTGGGTGCGATGCGCTGGAACTGTAGATGTTGTGACCCGAAACCATTTGAAACAGATAC	2491							
Db	135	ACGTGTGTTGGCTGTGAAGTGTGAACAAGGAAATGAGATACGCGCGCTATAAAAAAGTAA	194							
QY	2492	GGGTG-----TTTGTGCAACCTGTGTGTGTCTACTGCAAGTACATTAAGGCTCTA	2545							
Db	195	AAAAGTAACATTAACGTGGGCTCTTTTAACTGACGAAACGAACTTGAACGATCTA	254							
QY	2546	CGAGGGCTTTTCAAACGCAACGCTGTGGCCCTCTTTTCCAGATTTGAATTTACTCCGT	2605							
Db	255	CAACCAATTTCCAAATGCCGTTCTGTGGCCCGTTTTCATTATGCGTCAATGATGTGACA	314							
QY	2606	GTACAACACCGATTTGGTGGCATGCGTTTGGGGAAGTAACTCAAGTCCGTGAAGCGT	2665							
Db	315	ATTTCAGCGTCTGCGCTGGAGACGCAATCTAACCGGTAAATGCGTGTGCGAGTAAATT	374							
QY	2666	GAGCGAAGTGGCGCGAACACGAGTGGCACTGTGTGGGTCAAGACTATACGCTGTGCGT	2725							
Db	375	ACTGCGCGCTGTGCAACACGATGACATTAATCTGGAATCAACGATTAATACCGTGGCCATT	434							
QY	2726	TCTGGCATTTTGGCGCCAGATGCGCCCTGATTTTAAAGATCGGTTTCTTCCCTCCCATTC	2785							
Db	435	TGCGCATGAATTACGCAAAACGGGAGTGAATATGCAATGGTGTCTTTCGTGCAATATTC	494							
QY	2786	CTTCCCTTCCCGATCGTGTCCGTACAGCTGC	2817							
Db	495	TTTCCCGACACCGGAATCTTCAAGGCGTGC	526							

RESULT 8  
 US-08-274-121B-1  
 Sequence 1, Application US/08274121B  
 Patent No. 6133034  
 GENERAL INFORMATION:  
 APPLICANT: Arne Reidar Strom  
 APPLICANT: Inga Kaasen  
 APPLICANT: Olaf Bay Styrvold  
 APPLICANT: John McDougall  
 TITLE OF INVENTION: Methods and Compositions  
 TITLE OF INVENTION: Related To The Production  
 TITLE OF INVENTION: of Trehalose  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Calgene, Inc.  
 STREET: 1920 Fifth Street  
 CITY: Davis  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 95616  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Disquette, 3.50 inch, 2.0 MB  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Macintosh 7.1  
 SOFTWARE: Microsoft Word 5.1(a)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/274,121B  
 FILING DATE: 12-JULY-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/893,099  
 FILING DATE: 27-MAY-1992  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Elizabeth Lassen  
 REGISTRATION NUMBER: 31,845  
 NAME: Donna F. Scherer  
 REGISTRATION NUMBER: 34,719

REFERENCE/DOCKET NUMBER: CGNE 86 (1)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (916) 753-6313  
TELEFAX: (916) 753-1510  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2868 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
US-08-274-121B-1

Query Match 2.5%; Score 71.6; DB 3; Length 2868;  
Best Local Similarity 49.1%; Pred. No. 2e-12;  
Matches 222; Conservative 0; Mismatches 224; Indels 6; Gaps 1;

2372 CTCCCGCAGCCCGGCTGCTGTCAGCGGCTTTCCCGCTTGGACAAACATCGTG 2431  
1500 CGCGCCAGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1559  
2432 ATGTGGGTCGATGCGCTGGAATGATGTTGCAACCCGACATTTGCAACAGATAC 2491  
1560 ACTGTGTTGGCTGAGTGGTGAACAGGAAATGAGATGAGCGCTAAAGGTGAA 1619  
2492 GGGT-----TTTGTGTCACCTCTGTCTTCTACTGCAAGTACTATGAGGCTTCTA 2545  
1620 AAAAGTAACTTACGTGGGCTCTTTTAACTTCAGCAACAGACCTTGAACAACTA 1679  
2546 CGAGGCTTTTCAACGCAACGCTGCTGCTCTTTTCCAGATTTGATTTACTCCGGT 2605  
1680 CAACCAATTCCTCAATGCCCTCTCTGCGCCGCTTTTCAATTTGCGCTGCAATCTG 1739  
2606 GTACACACGATGTTGTCGATGCTTTCGGAAGTAACTCAAGTTCCTGAAGCGT 2665  
1740 ATTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1799  
2666 GAGCCAGTGGCGGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2725  
1800 ACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1859  
2726 TCTGCGATTTTGGCGCAGATGCGCCTGATTTGAAATGCTTCTTCTCCACATTC 2785  
1860 TGGCATGATTTACGAAAGGAGTGAATATCCCATTTGTTCTTCTGCAATTC 1919  
2786 CTTCCTTCCCTGATCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2817  
1920 TTTCGCGACCGGAATCTTCAACGCGCTGC 1951

## RESULT 9

US-09-489-039A-7037  
Sequence 7037, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 7037  
LENGTH: 1479  
TYPE: DNA  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-7037

Query Match 2.5%; Score 70.2; DB 4; Length 1479;  
Best Local Similarity 52.6%; Pred. No. 3.4e-12;  
Matches 153; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

2516 CCTACTGCAAGTACTATGAAGGCTTACAGAGGCTTTCAACGCAACGCTGCGCC 2575  
255 CTTATGAAAGGAGCATGATGATTAATTAACCAAGTCTCTTAACGCGCTGCTGCGC 314  
2576 TCTTTCCAGATTTGATTTGTTACTCCGCTGTAACAACCCATGTTGGATGCTTTCG 2635  
315 GCGTTCCATGATGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 374  
2636 GGAAGTAACTCAAGTTCGTTGAAGCCGTGAGCCAAAGTGCAGCAGGTCGACATGT 2695  
375 GCGGTTAAGCGCATGCTGCGGGAACAAGCTTCTGCTGCTGCTGCTGCTGCTGCTG 434  
2696 GTGGTGCAGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2755  
435 GTGATCATGATTAATCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 494  
2756 TTGAAAGTGGTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2806  
495 CAATCGATCGGGTTTCTTCAATATTCGTTCCGACGCGGAGATTTT 545

## RESULT 10

US-09-328-352-595  
Sequence 595, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 595  
LENGTH: 1455  
TYPE: DNA  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-595

Query Match 2.0%; Score 56; DB 4; Length 1455;  
Best Local Similarity 49.7%; Pred. No. 1.7e-07;  
Matches 143; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

2530 ACTATGAAGCTTTCTACGAGGCTTTTCAACGCAACGCTGCTCTTTTCAACGATT 2589  
242 AATATGCAAGTACTACTGCTGTTTGGCAATTAAGTATTAATGCTGCTGCTGCTGCT 301  
2590 TGAATGTAATCTCCGCTGTAACAACCGATGCTGCTGCTGCTGCTGCTGCTGCTG 2649  
302 GGGATGACCTGATGCAATTAATGAGAGAAATATATACCTACCAAAAGTCAATGCTT 361  
2650 AGTTGCTGAAGCCGTGAGCCAAAGTGGCGGACACGCTGCCACTGTGTGGTGCAGACT 2709  
362 TATTGCTGAAAATAATTAACAAGATTTGCTCAAGCTGATGCTGATTTGGTGCATGACT 421  
2710 ATCAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2769  
422 ATCACTTTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481  
2770 TCTTCTCCACATTCCTTCCCTTCCCTGATCTGCTGCTGCTGCTGCTGCTGCTGCT 2817  
482 TCTTTTGCATATTCCTTTCGCAAGCTTAATATCTGGGCAAGATCC 529

## RESULT 11

US-09-651-169A-36  
Sequence 36, Application US/09651169A  
Patent No. 6506565  
GENERAL INFORMATION:  
APPLICANT: Comer, Timothy W  
TITLE OF INVENTION: Plant Regulatory Sequences for Selective Control of Gene Expressi

FILE REFERENCE: 06009.0019.NPUS00 (RENN.019)  
CURRENT APPLICATION NUMBER: US/09/651,169A  
CURRENT FILING DATE: 2000-08-30  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 36  
LENGTH: 654  
TYPE: DNA  
ORGANISM: Zea Mays  
US-09-651-169A-36

Query Match  
Best Local Similarity 51.4%; Pred. No. 4e-05;  
Matches 108; Conservative 1; Mismatches 101; Indels 0; Gaps 0;

QY 2608 ACAACACCGATGTTGGCATGCGTTTGGGAGTAACCTCAAGTTGCTGAACCGGTGA 2667  
DB 359 ACCGACGCGTTGGAGAGCGTACTGCTCGCAACAGTTCTTCTTGAGAGAGTCTGCG 418  
QY 2668 GCCAAGTGGCGGACACGCGTGCACCTGTGTGGTGCAGACTATCAGCTGTGTGTTG 2727  
DB 419 AGGATATCAACCGGAGAGATGACTATGTTGGGTTCACGACTACATCTCATGGCGCTGC 478  
QY 2728 CTGGCATTTTGGCGGACAGATGGCGCCCTGATTTGAAGATCGGTTTCTCTCCACATTCCT 2787  
DB 479 CTACCTTCTCGCGGCTGCTTCAACCGCCTCCGCAATGGAATTTCTCTCCACACCCCT 538  
QY 2788 TCCCTTCCCTGATCTGTTCGTCAGCTGC 2817  
DB 539 TCCCTCTCGGAGATCTACGCAACCCCTCC 568

RESULT 12  
US-08-232-463-14  
Sequence 14, Application US/08232463  
Patent No. 3670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESS: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0239  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE: EP 91 114 300.6  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELEPHONE: (703) 836-9300  
TELEFAX: (703) 683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:

LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZ9pt-Fls  
US-08-232-463-14

Query Match  
Best Local Similarity 1.7%; Score 47.6; DB 1; Length 7218;  
Matches 14; Conservative 218; Mismatches 162; Indels 0; Gaps 0;

QY 1175 GCTCCGGTACAGACGATGTCAGATTTTGAACACTCCTGTTTACCGCGGCGATGTT 1234  
DB 1042 GCTGACAGTGAAGGAGCTGTCATATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1101  
QY 1235 GCTGGCGGTGGTTGGGCAATTCAGCTTTCGAATCTGTGATGTCATGTCGCGCATG 1294  
DB 1102 TT 1161  
QY 1295 GAGTCGCTGACGACCTAATTAATCGTCTACATTCGCCGCAATTAATGCTGAGCGTC 1354  
DB 1162 TT 1221  
QY 1355 ACCGACGCGCTTTCGACGAGTGTGTTAGCGGAGTGTGCTGATTAATGCGGGG 1414  
DB 1222 TT 1281  
QY 1415 CTACTGCGCTGATGAGTTCGCTTAACTCTGTTTAACTGTTTAAAGCCCGTC 1474  
DB 1282 TT 1341  
QY 1475 TCTGCGCTGATGCTGCAACAGACGATTTGTTTCACTGCTGATGTTGCTGCGCTGA 1534  
DB 1342 TT 1401  
QY 1535 TTCTTGATTCACGCTGATGTTGCGCATGCGC 1568  
DB 1402 TT 1435

RESULT 13  
US-09-198-452A-1  
Sequence 1, Application US/09198452A  
Patent No. 6559294  
GENERAL INFORMATION:  
APPLICANT: Griffiths, R.  
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
FILE REFERENCE: 9710-003-999  
CURRENT APPLICATION NUMBER: US/09/198,452A  
CURRENT FILING DATE: 1998-11-24  
NUMBER OF SEQ ID NOS: 6849  
SEQ ID NO 1  
LENGTH: 1230025  
TYPE: DNA  
ORGANISM: Chlamydia pneumoniae  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)..(15000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (15001)..(30000)  
OTHER INFORMATION: n=a or c or g or t  
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NAME/KEY: misc feature  
LOCATION: (60001)..(75000)

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47	NAME/KEY: misc feature
48	LOCATION: (300001)..(315000)
49	OTHER INFORMATION: n=a or c or g or t
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51	LOCATION: (315001)..(330000)
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60	LOCATION: (360001)..(375000)
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72	LOCATION: (420001)..(435000)
73	OTHER INFORMATION: n=a or c or g or t

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NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (600001) ..(615000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
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LOCATION: (795001)..(810000)  
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NAME/KEY: misc feature  
LOCATION: (885001)..(900000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (900001)..(915000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature

Query Match 1.6%; Score 45.8; DB 4; Length 1230025;  
Best Local Similarity 76.7%; Pred. No. 0.087;  
Matches 56; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 179 GCTGAGAGAGACTGTAAGTCTCAAGCTTACAGTGGCTGGCTGCAATTG 238  
DB 303710 GCTGAGAGAGAGAAATTAAGCCCTCAACCGTTGATTACAAATGCTCTGCCAATTG 303769  
QY 239 CGCCACTCCAGCA 251  
DB 303770 AGCTACTCCAGCA 303782

RESULT 14  
US-08-956-171E-4023  
Sequence 4023, Application US/08956171E  
Patent No. 6593114  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
Gill H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 4023:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 381 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 4023:  
US-08-956-171E-4023

Query Match 1.6%; Score 45.6; DB 4; Length 381;  
Best Local Similarity 73.1%; Pred. No. 0.0016;  
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 174 ATTGAGCTGAGAGAGACTGTAAGTCTCAAGCTTACAGTGGCTGGCTGCC 233  
DB 87 ATGAGCGAGGAGAGAGACTGTAAGCCCAACCTACTGATTACAAAGTCAGTTGCTTACC 146  
QY 234 AATTGCCCACTCCAGCA 251  
DB 147 AATTGAGCTAGGCCGCA 164

RESULT 15  
US-08-956-171E-4234/C  
Sequence 4234, Application US/08956171E  
Patent No. 6593114  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
Gill H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 4234:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 400 base pairs  
TYPE: nucleic acid

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; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4234:
US-08-956-171E-4234

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Query Match      1.6%; Score 44.8; DB 4; Length 400;
Best Local Similarity 61.9%; Pred.No.0.00031;
Matches 70; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 155 ACCCCTTGACCTGCTGTATTGAGCTGGAGAGAGACTTGAACCTCACTCAAGCATT 214
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Db 293 ANTGCTTACCCCTCCATAAATGGTCCGGCCAGAGACTTGAACCCCAACTCTGATT 234
   |||||

QY 215 ACAAGTGGCTGCGCTGCCAATTGGCCCACTCCAGCACCGCAGATGCTGATGA 267
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-963-521-1

Perfect score: 2817

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Scoring table:

IDENTITY NUC  
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Searched:

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Minimum DB seq length: 0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2817	100.0	2817	9	US-09-951-536-1 Sequence 1, Appli
2	2817	100.0	2817	9	US-09-963-521-1 Sequence 1, Appli
3	2817	100.0	2817	9	US-09-834-721-1 Sequence 1, Appli
4	2817	100.0	2817	9	US-09-783-388-1 Sequence 1, Appli
5	2817	100.0	2817	10	US-09-951-535-1 Sequence 1, Appli
6	2817	100.0	2817	17	US-10-224-574-9 Sequence 1, Appli
7	2783.4	98.8	3309400	9	US-09-738-626-1 Sequence 1, Appli
8	1836.6	65.2	13909	9	US-09-951-536-1 Sequence 3, Appli
9	1836.6	65.2	13909	9	US-09-963-521-3 Sequence 3, Appli
10	1836.6	65.2	13909	9	US-09-834-721-3 Sequence 3, Appli
11	1836.6	65.2	13909	9	US-09-783-388-3 Sequence 3, Appli
12	1836.6	65.2	13909	10	US-09-951-535-3 Sequence 3, Appli
13	1836.6	65.2	13909	17	US-10-224-574-11 Sequence 11, Appli
14	1561.2	55.4	1590	13	US-10-627-476-557 Sequence 557, App

15	1561.2	55.4	1590	13	US-10-450-055-41	Sequence 41, Appli
16	1474.2	52.3	1503	9	US-09-738-626-2884	Sequence 2884, Ap
17	1405.6	49.9	3010	14	US-10-058-945-1	Sequence 1, Appli
18	969.6	34.4	2369	9	US-09-895-382-29	Sequence 29, Appli
19	625.8	22.2	1578	13	US-10-450-055-29	Sequence 29, Appli
20	525.8	18.7	1455	9	US-09-738-626-2886	Sequence 2886, Ap
21	327	11.6	327	9	US-09-738-626-2885	Sequence 2885, Ap
22	157.8	5.6	1503	9	US-09-712-363-128	Sequence 128, App
23	111.2	3.9	1446	16	US-10-369-493-39221	Sequence 39221, A
24	111.2	3.9	1446	16	US-10-369-493-39666	Sequence 39666, A
25	111.2	3.9	1446	16	US-10-369-493-40025	Sequence 40025, A
26	96.2	3.4	1377	16	US-10-369-493-42956	Sequence 42956, A
27	89.4	3.2	261	9	US-09-867-550-445	Sequence 445, App
28	81.8	2.9	1362	16	US-10-369-493-41490	Sequence 41490, A
29	80.2	2.8	1359	16	US-10-369-493-28393	Sequence 28393, A
30	80.2	2.8	1407	16	US-10-369-493-31152	Sequence 31152, A
31	75.8	2.7	1368	16	US-10-369-493-31089	Sequence 31089, A
32	75.8	2.7	1407	16	US-10-369-493-28331	Sequence 28331, A
33	74.4	2.6	1323	16	US-10-369-493-37290	Sequence 37290, A
34	74.2	2.6	1356	16	US-10-369-493-39284	Sequence 39284, A
35	74.2	2.6	1356	16	US-10-369-493-39661	Sequence 39661, A
36	74.2	2.6	1356	16	US-10-369-493-40023	Sequence 40023, A
37	72.2	2.6	536165	10	US-09-939-964-1	Sequence 1, Appli
38	71.6	2.5	1425	16	US-10-369-493-24561	Sequence 24561, A
39	71.6	2.5	1425	16	US-10-369-493-24561	Sequence 1, Appli
40	71.2	2.5	1450	17	US-10-369-493-26438	Sequence 26438, A
41	69.8	2.5	1448	16	US-10-369-493-44630	Sequence 44630, A
42	68.2	2.4	1374	16	US-10-369-493-28062	Sequence 28062, A
43	68.2	2.4	1374	16	US-10-369-493-30816	Sequence 30816, A
44	66.2	2.4	1389	15	US-10-156-761-3920	Sequence 3920, Ap
45	66.2	2.4	9025608	15	US-10-156-761-1	Sequence 1, Appli

#### ALIGNMENTS

RESULT 1  
US-09-951-536-1  
Sequence 1, Application US/09951536  
Patent No. US20020107378A1  
GENERAL INFORMATION:  
APPLICANT: ZIEGLER, PETRA  
APPLICANT: EGGELING, LOTMAR  
APPLICANT: SAHM, HERMANN  
APPLICANT: THIERBACH, GEORG  
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND  
PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE  
TITLE OF INVENTION: USING CORNEFORM BACTERIA  
FILE REFERENCE: 21123/282414/MAS  
CURRENT APPLICATION NUMBER: US/09/951,536  
CURRENT FILING DATE: 2001-09-14  
PRIOR APPLICATION NUMBER: 09/431,099  
PRIOR FILING DATE: 1999-11-01  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 2817  
TYPE: DNA  
ORGANISM: Corynebacterium glutamicum  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (398)..(1864)  
OTHER INFORMATION: three-Gen  
US-09-951-536-1

Query Match 100.0%; Score 2817; DB 9; Length 2817;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAATATATCCCGCCACCACTGGCGCATTCACCGCTTCATTTCCAAATATG 60  
DB 1 AATGAATATATCCCGCCACCACTGGCGCATTCACCAACCGCTTCATTTCCAAATATG 60

QY 61 AGCCAAAGGAAAAAGAAAGCCCTAAGCCCGGTGTTAATGAGACATCTTTGAGACC 120  
DB 61 AGCCAAAGGAAAAAGAAAGCCCTAAGCCCGGTGTTAATGAGACATCTTTGAGACC 120  
QY 121 TCAAGCCAAAAAGGGGATTTTTCATTAAAGAAATATACCCCTTGACCTGGTATTAGC 180  
DB 121 TCAAGCCAAAAAGGGGATTTTTCATTAAAGAAATATACCCCTTGACCTGGTATTAGC 180  
QY 181 TGGAGAGAGACTGTAAGCTCTCAACCTTACGATTAACAAGTGGCTGGTCCCAATTCG 240  
DB 181 TGGAGAGAGACTGTAAGCTCTCAACCTTACGATTAACAAGTGGCTGGTCCCAATTCG 240  
QY 241 CCACTCCAGACCGGAGATGCTGATGATCAACATTAAGAAATAGTATCTTAAGGTATGT 300  
DB 241 CCACTCCAGACCGGAGATGCTGATGATCAACATTAAGAAATAGTATCTTAAGGTATGT 300  
QY 301 GTATATCAATCAATGGAATTCGGGGGCTAGAGTCTGGTGAACCGTGCAATTAACACTGTG 360  
DB 301 GTATATCAATCAATGGAATTCGGGGGCTAGAGTCTGGTGAACCGTGCAATTAACACTGTG 360  
QY 361 ATTGGAATCTTTTCTCTGCAAAATGTTTTCAGCGAGATGTTGAGTTTGGACCTTTCG 420  
DB 361 ATTGGAATCTTTTCTCTGCAAAATGTTTTCAGCGAGATGTTGAGTTTGGACCTTTCG 420  
QY 421 TGGCCGATTTCAAGATTGACGCTGCAAAAGCCGCACTCCGCGCATGCGCACTAGCCCC 480  
DB 421 TGGCCGATTTCAAGATTGACGCTGCAAAAGCCGCACTCCGCGCATGCGCACTAGCCCC 480  
QY 481 GATTGATCTCTACTACCAATGATCAAGTGGCGGTGATGATTTGGCTGCGAGAAATGG 540  
DB 481 GATTGATCTCTACTACCAATGATCAAGTGGCGGTGATGATTTGGCTGCGAGAAATGG 540  
QY 541 CGATATTTTGTCTTCTTCAAGGTAAGTCAAAAGTATTAACAAGTGAAGTTGAGCGGT 600  
DB 541 CGATATTTTGTCTTCTTCAAGGTAAGTCAAAAGTATTAACAAGTGAAGTTGAGCGGT 600  
QY 601 GACCTCTGCTATGAGCTGTACTATACGATGATGATATCAAGTGAATTAAGATCAAT 660  
DB 601 GACCTCTGCTATGAGCTGTACTATACGATGATGATATCAAGTGAATTAAGATCAAT 660  
QY 661 CTTACCAAAACATCGGTGAGAGAGAAAGTCCGCGTCAACGTGTTCAATGTTGGGCA 720  
DB 661 CTTACCAAAACATCGGTGAGAGAGAAAGTCCGCGTCAACGTGTTCAATGTTGGGCA 720  
QY 721 GTTGAACAACAATCTCTCAAACTGTCTGAGGTGACCGTTGATCCGTTCAATTCAGGC 780  
DB 721 GTTGAACAACAATCTCTCAAACTGTCTGAGGTGACCGTTGATCCGTTCAATTCAGGC 780  
QY 781 TGGTGTACCCCGCTGAGAGTTCGAGAAATTTCTGACGAGTTGAGACATTCGCTGC 840  
DB 781 TGGTGTACCCCGCTGAGAGTTCGAGAAATTTCTGACGAGTTGAGACATTCGCTGC 840  
QY 841 GTCTTATGTTTCCCGTGTGCGTGTGCTGAGGAGATGATGAGGTGAGCTGTGCTGT 900  
DB 841 GTCTTATGTTTCCCGTGTGCGTGTGCTGAGGAGATGATGAGGTGAGCTGTGCTGT 900  
QY 901 GCTGTGTTGGTGTGATGAGGAGGTTCCTTAATGCTTTTATTAACCGGCTTACATCAT 960  
DB 901 GCTGTGTTGGTGTGATGAGGAGGTTCCTTAATGCTTTTATTAACCGGCTTACATCAT 960  
QY 961 TGGCAGAGATCATTTTGGGAAAGAAAGGTTTGGCTACTTCTTCCAAATTTGTG 1020  
DB 961 TGGCAGAGATCATTTTGGGAAAGAAAGGTTTGGCTACTTCTTCCAAATTTGTG 1020  
QY 1021 TGGTTTATTTGACAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1080  
DB 1021 TGGTTTATTTGACAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1080  
QY 1081 TGAAGATCAAAACGAGCGAGATCAATGATGATGATGATGATGATGATGATGATGAT 1140  
DB 1081 TGAAGATCAAAACGAGCGAGATCAATGATGATGATGATGATGATGATGATGATGAT 1140  
QY 1141 ACTTGTGCAATCTCTGAGAGAGGATCAAGGCGCTCGGTGACAGCAAGTGCAGATT 1200

DB 1141 ACTTGTGCAATCTCTGAGAGAGGATCAAGGCGCTCGGTGACAGCAAGTGCAGATT 1200  
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DB 1201 TTTTGAACAACCTCTGTTTACCGCGCGCATTTGTTGCTGGGTGGTTTGGGCAATTCAGCT 1260  
QY 1261 TTTGGAATCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320  
DB 1261 TTTGGAATCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320  
QY 1321 GTCTACATTCGCGCGCATTAATGCTGTGAGTCAACGAGCGGCTTCCGAGTGGGTTG 1380  
DB 1321 GTCTACATTCGCGCGCATTAATGCTGTGAGTCAACGAGCGGCTTCCGAGTGGGTTG 1380  
QY 1381 TTAACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
DB 1381 TTAACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
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DB 1441 TTAATACCTCTGTTGTTTATTAAGGCGCGCTCTGCGCGCTGATGATGATGATGATGAT 1500  
QY 1501 AGTTGTTTCACTGTGTTGCTTTCGCGCTGATGATGATGATGATGATGATGATGATGAT 1560  
DB 1501 AGTTGTTTCACTGTGTTGCTTTCGCGCTGATGATGATGATGATGATGATGATGATGAT 1560  
QY 1561 GATTGCGGATCAACCAATGCTTCAAGTCTGACATTTACCGGAGATGATGATGATGATGAT 1620  
DB 1561 GATTGCGGATCAACCAATGCTTCAAGTCTGACATTTACCGGAGATGATGATGATGATGAT 1620  
QY 1621 CTTGAATGATCAAAACATCATGAGGTTTCAACCAATGCGGTGTTTACGCACTGCTTC 1680  
DB 1621 CTTGAATGATCAAAACATCATGAGGTTTCAACCAATGCGGTGTTTACGCACTGCTTC 1680  
QY 1681 ATCACTTCCGCTGCGGTGTTTGGGTGATGATGATGATGATGATGATGATGATGATGAT 1740  
DB 1681 ATCACTTCCGCTGCGGTGTTTGGGTGATGATGATGATGATGATGATGATGATGATGAT 1740  
QY 1741 AGCTTTCAACCAATGCGGTGATTTTACCAAGCGAATGATGATGATGATGATGATGATGAT 1800  
DB 1741 AGCTTTCAACCAATGCGGTGATTTTACCAAGCGAATGATGATGATGATGATGATGATGAT 1800  
QY 1801 TGAAGAGATCAAGCGCGGAGAGAAAGTCCAAAGATTAACAAAGTGTGATTA 1860  
DB 1801 TGAAGAGATCAAGCGCGGAGAGAAAGTCCAAAGATTAACAAAGTGTGATTA 1860  
QY 1861 AAGTAAATCAACCTGTTAGGCTCTTTCGTTAATTAAGCTAATTAAGCTAATTAAGCT 1920  
DB 1861 AAGTAAATCAACCTGTTAGGCTCTTTCGTTAATTAAGCTAATTAAGCTAATTAAGCT 1920  
QY 1921 TGGCTTTAAACATCAAGAGATCTTTCGCGGCAAAATCAAGAGATCTTTCGCGGCA 1980  
DB 1921 TGGCTTTAAACATCAAGAGATCTTTCGCGGCAAAATCAAGAGATCTTTCGCGGCA 1980  
QY 1981 CAGAAATCCCTTCAAGCTGTTGAAGAGAAACCGACCGGCTGCGGAGATTTGTTGCA 2040  
DB 1981 CAGAAATCCCTTCAAGCTGTTGAAGAGAAACCGACCGGCTGCGGAGATTTGTTGCA 2040  
QY 2041 CCTATTCTAAGAGATCTTTCGAGGCGTCACTTGAATGATGATGATGATGATGATGATGAT 2100  
DB 2041 CCTATTCTAAGAGATCTTTCGAGGCGTCACTTGAATGATGATGATGATGATGATGATGAT 2100  
QY 2101 AAGGCTGTGTTTACCAAGAGTCTTTCGAGGAGAGAGAGTTCAGCCAAAGAGCTTA 2160  
DB 2101 AAGGCTGTGTTTACCAAGAGTCTTTCGAGGAGAGAGAGTTCAGCCAAAGAGCTTA 2160  
QY 2161 CAAAGCGATCTGTAAGGACCAAGCTAAGAGAGCTGTGCTAAGAGAGAGAGAGAGAG 2220  
DB 2161 CAAAGCGATCTGTAAGGACCAAGCTAAGAGAGCTGTGCTAAGAGAGAGAGAGAGAG 2220  
QY 2221 CCACTAAGAAATCTACTAAGAAACCAACCGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 2280

Db	2221	CCACTAAGAAACTACTTAAAAAGACCAACCGCAAGAGACCAAAAGAGCTTTAAGCCG	2280
QY	2281	GATCTTATATAGATGATATCCATAGCTTTGATGTTGTCATACCGTCGCAAGATTA	2340
Db	2281	GATCTTATATAGATGATATCCATAGCTTTGATGTTGTCATACCGTCGCAAGATTA	2340
QY	2341	TGACTGTCCACCCAGATGGTAGCTATAGATCTCCCCAGCCCGGTGGCTTGTACGG	2400
Db	2341	TGACTGTCCACCCAGATGGTAGCTATAGATCTCCCCAGCCCGGTGGCTTGTACGG	2400
QY	2401	GGGCTTCCCCCGCTTCGGAACAACATCGTGATGTTGGGTGGATGGCTTGGAACTGTAG	2460
Db	2401	GGGCTTCCCCCGCTTCGGAACAACATCGTGATGTTGGGTGGATGGCTTGGAACTGTAG	2460
QY	2461	ATGTTCACCCCGACCACTTTGCAACAGATACGGGTGTTTGTGTGACCCCTTGTCTCA	2520
Db	2461	ATGTTCACCCCGACCACTTTGCAACAGATACGGGTGTTTGTGTGACCCCTTGTCTCA	2520
QY	2521	CTGCAAGTACTATAGAGGCTCTACGAGGGCTTTTGAAGCAACGTGTGGCTCTTT	2580
Db	2521	CTGCAAGTACTATAGAGGCTCTACGAGGGCTTTTGAAGCAACGTGTGGCTCTTT	2580
QY	2581	TCACAGATTGATGTGTAATCTCCGCTGTGCAACACCGATTGGTGGCATGCTTCCGAGAG	2640
Db	2581	TCACAGATTGATGTGTAATCTCCGCTGTGCAACACCGATTGGTGGCATGCTTCCGAGAG	2640
QY	2641	TAAACCTCAAGTGGCTGAAGCCGAGACCCAAAGTGGCGGCAACGGTGGCACTGTGGG	2700
Db	2641	TAAACCTCAAGTGGCTGAAGCCGAGACCCAAAGTGGCGGCAACGGTGGCACTGTGGG	2700
QY	2701	TGCAGAGCTATCAGCTGTGTGCTGTGTTCTCGCATTTTGGCGCAGATCGCCCTGATTTGA	2760
Db	2701	TGCAGAGCTATCAGCTGTGTGCTGTGTTCTCGCATTTTGGCGCAGATCGCCCTGATTTGA	2760
QY	2761	AGATGGTTCTTCTCTCCACATTCCTTCCCTTCCCTGATCTGTTCGTAGCTGC	2817
Db	2761	AGATGGTTCTTCTCTCCACATTCCTTCCCTTCCCTGATCTGTTCGTAGCTGC	2817
RESULT 2			
US-09-963-521-1 ; Sequence 1, Application US/09963521			
; Patent No. US30020146781A1			
; GENERAL INFORMATION:			
; APPLICANT: ZIEGLER, PETRA			
; APPLICANT: EGGELING, IOTHAR			
; APPLICANT: SAHM, HERMANN			
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE			
; TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF			
; FILE REFERENCE: L-THREONINE USING CORYNEFORM BACTERIA			
; CURRENT APPLICATION NUMBER: US/09/963,521			
; CURRENT FILING DATE: 2001-09-27			
; PRIOR APPLICATION NUMBER: 09/431,099			
; PRIOR FILING DATE: 1999-11-01			
; PRIOR APPLICATION NUMBER: DE 199 41 478.5			
; PRIOR FILING DATE: 1999-09-01			
; NUMBER OF SEQ ID NOS: 10			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 1			
; LENGTH: 2817			
; TYPE: DNA			
; ORGANISM: Corynebacterium glutamicum			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (398)..(1864)			
; OTHER INFORMATION: thrE-Gen			
US-09-963-521-1			

QY	1	AATGAATAAT	CCCCTTACCA	CACTGCGCA	CACTTCAAC	CACCGTTTCA	TTTCCAAACATCG	60
Db	1	AATGAATAAT	CCCCTTACCA	CACTGCGCA	CACTTCAAC	CACCGTTTCA	TTTCCAAACATCG	60
QY	61	AGCCAAAGGAAAA	AGAAAGCCCTTA	AGCCCGCTGT	ATTAAATGAGA	CTTTTGGAGACC	120	
Db	61	AGCCAAAGGAAAA	AGAAAGCCCTTA	AGCCCGCTGT	ATTAAATGAGA	CTTTTGGAGACC	120	
QY	121	TCAAGCCAAA	AAAGGGGCA	ATTTCATTA	AGAAAATA	CCCCCTTGA	CCGCGGTATTTGAGC	180
Db	121	TCAAGCCAAA	AAAGGGGCA	ATTTCATTA	AGAAAATA	CCCCCTTGA	CCGCGGTATTTGAGC	180
QY	181	TGGAGAAAGAG	ACTTGAAC	CTCTCAAC	CTTACAGATTA	CAAGTGCCTTG	CGCCCAATTGCG	240
Db	181	TGGAGAAAGAG	ACTTGAAC	CTCTCAAC	CTTACAGATTA	CAAGTGCCTTG	CGCCCAATTGCG	240
QY	241	CCACTCCAGA	CCGCGAGT	CTCATATG	ATCAACAACTA	CGAATACG	ATCTTTAGCGATGT	300
Db	241	CCACTCCAGA	CCGCGAGT	CTCATATG	ATCAACAACTA	CGAATACG	ATCTTTAGCGATGT	300
QY	301	GTCATTCACA	TGAATGGA	ATTCGGGGCT	AGATTCGGTGA	ACCGTGGATTA	ACGACCTGTG	360
Db	301	GTCATTCACA	TGAATGGA	ATTCGGGGCT	AGATTCGGTGA	ACCGTGGATTA	ACGACCTGTG	360
QY	361	ATTGAACTCT	TTTTCCTTG	CAAAATGTTT	TCAGCGGA	TGTTGAGTTT	GCACCCCTTG	420
Db	361	ATTGAACTCT	TTTTCCTTG	CAAAATGTTT	TCAGCGGA	TGTTGAGTTT	GCACCCCTTG	420
QY	421	TGGCCGCAT	TTTCAACAG	TGTGAGCG	CTGCAAAAG	CCGCACTCCG	CCATGCGCACTAGCCCC	480
Db	421	TGGCCGCAT	TTTCAACAG	TGTGAGCG	CTGCAAAAG	CCGCACTCCG	CCATGCGCACTAGCCCC	480
QY	481	GATTGAATCT	CACGCA	CCATAGTCA	AGTGGCCGGTGA	GAATTTGGCTG	CCGAGAAATTGG	540
Db	481	GATTGAATCT	CACGCA	CCATAGTCA	AGTGGCCGGTGA	GAATTTGGCTG	CCGAGAAATTGG	540
QY	541	CGAATATTT	GCTTCTT	CAGTACGT	CAAAACAGTGA	TACCAAGTCA	AGTTCGACGGGT	600
Db	541	CGAATATTT	GCTTCTT	CAGTACGT	CAAAACAGTGA	TACCAAGTCA	AGTTCGACGGGT	600
QY	601	GACCTCTGG	GTATGG	CTCTGTA	CTAATACG	ATGATCA	CGTTGAATACGATCA	660
Db	601	GACCTCTGG	GTATGG	CTCTGTA	CTAATACG	ATGATCA	CGTTGAATACGATCA	660
QY	661	CTTCAACCA	ATCCGGTGA	GAGGAAGA	TGCCCGGTCA	CCGTTTCA	TGTTGGGCA	720
Db	661	CTTCAACCA	ATCCGGTGA	GAGGAAGA	TGCCCGGTCA	CCGTTTCA	TGTTGGGCA	720
QY	721	GTTGACACCA	ACTTCTCCAA	ACTCTG	AGGTTACCG	TTGATCCG	TTCCATTCA	780
Db	721	GTTGACACCA	ACTTCTCCAA	ACTCTG	AGGTTACCG	TTGATCCG	TTCCATTCA	780
QY	781	TGGTGTAC	CCCCGCTGA	GGTTG	CCGAGAAA	ATTCGAG	CAAGTTGAGCAATCG	840
Db	781	TGGTGTAC	CCCCGCTGA	GGTTG	CCGAGAAA	ATTCGAG	CAAGTTGAGCAATCG	840
QY	841	GTTTATGG	TTCCCTGT	TGGCTGT	TGGCTGG	CGCAATG	ATGATGCGCTGT	900
Db	841	GTTTATGG	TTCCCTGT	TGGCTGT	TGGCTGG	CGCAATG	ATGATGCGCTGT	900
QY	901	GCTGTGG	GGTGGAT	GGAGGTT	TCCCTA	TGCTTTAT	TACCGGTTCA	960
Db	901	GCTGTGG	GGTGGAT	GGAGGTT	TCCCTA	TGCTTTAT	TACCGGTTCA	960
QY	961	TGCCACG	ACGTATTT	TGGAAAA	GAAGGTT	TGCCTA	CTTCTTCCAAA	1020
Db	961	TGCCACG	ACGTATTT	TGGAAAA	GAAGGTT	TGCCTA	CTTCTTCCAAA	1020
QY	1021	TGGTTTAT	TGCGAC	CGCTCG	ATCGATG	ATTCCTT	TGGCGTTG	1080
Db	1021	TGGTTTAT	TGCGAC	CGCTCG	ATCGATG	ATTCCTT	TGGCGTTG	1080
QY	1081	TGAATCAAA	CCGAGCA	GATCAT	CGCATCTG	GAATTTGT	GTGTGGAGGTTGAC	1140

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1201 TTTTGAACACCTCTGTTTAAACCGCGGCAATTTGCTGCGTGGGTTTGGGCAATTCAGCT 1260  
1201 TTTTGAACACCTCTGTTTAAACCGCGGCAATTTGCTGCGTGGGTTTGGGCAATTCAGCT 1260  
1261 TTCTGAATCTTGAGATGATGATGCTGCGATGAGATGCGCTGACAGCACTTAATATTC 1320  
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1321 GTCTACATGCGCGCAATTAATCGCTGGTGGGCTGACCGAGCGGCTTTCGAGTGGGTTG 1380  
1381 TTACGCGAGTGTCTCTGATTTATTTGCGGGGCTTACTGCGCTGATGGGTTCTGGGTT 1440  
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1801 TGAGGAGATCAAGCGCGCGAGAGAAAGTCCAAAGACTAATCAAAAGTTGCTATATA 1860  
1861 AAGGTAAATCAACCTGCTTAAAGCGGCTTTGCTTAAATAGCGTGAATATCGGTCGA 1920  
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1981 CAGAAATCCCTTCAAGCTGTTTGAAGAGAAACGCAAGCGGTGCGCGAGATTTGTTGCA 2040  
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2161 CAAAGCGAGCTGTTAAG 2220

2161 CAAAGCGAGCTGTTAAG 2220  
2221 CCACTAAGAGAAATCTAATAAAG 2280  
2221 CCACTAAGAGAAATCTAATAAAG 2280  
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2701 TCGAGAGATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760  
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2761 AGAT 2817  
2761 AGAT 2817

RESULT 3  
US-09-834-721-1  
Sequence 1, Application US/09834721  
Patent No. US2002015551A1  
GENERAL INFORMATION:  
APPLICANT: RIEPING, MECHTILD  
TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE  
FILE REFERENCE: 21123/280169/MAS  
CURRENT APPLICATION NUMBER: US/09/834,721  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: DE 100 26 494.8  
PRIOR FILING DATE: 2000-05-27  
PRIOR APPLICATION NUMBER: DE 101 02 823.7  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 2817  
TYPE: DNA  
ORGANISM: Corynebacterium glutamicum  
FEATURE:  
OTHER INFORMATION: ATCC14752  
NAME/KEY: CPS  
LOCATION: (398)..(1864)  
OTHER INFORMATION: this gene  
US-09-834-721-1  
Query Match 100.0%; Score 2817; DB 9; Length 2817;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAATATATCCCTCTACCAACTGGCGATTTCAAACCGTTTCATTTCCAAACATCG 60  
Db 1 AATGAAATATCCCTCTACCAACTGGCGATTTCAAACCGTTTCATTTCCAAACATCG 60  
QY 61 AGCCNAGGGAAAAGAGCCCTTAGCCCGGTATTAATAGAGACTCTTTGGAGACC 120  
Db 61 AGCCNAGGGAAAAGAGCCCTTAGCCCGGTATTAATAGAGACTCTTTGGAGACC 120  
QY 121 TCAAGCCAAAAGGGGCAATTTTCATTTAGAAAATACCCCTTTGACCTGTATTTAGC 180  
Db 121 TCAAGCCAAAAGGGGCAATTTTCATTTAGAAAATACCCCTTTGACCTGTATTTAGC 180  
QY 181 TGGAGAAAGACTTGAATCTTCAACTTACCTTACGATTTCAAGTGGCTTGGCTGCAATTGCG 240  
Db 181 TGGAGAAAGACTTGAATCTTCAACTTACGATTTCAAGTGGCTTGGCTGCAATTGCG 240  
QY 241 CCACCTCCAGCAGCGAGATGCTGATCAACAACCTAGCAATAGCATTTAGGCTATGT 300  
Db 241 CCACCTCCAGCAGCGAGATGCTGATCAACAACCTAGCAATAGCATTTAGGCTATGT 300  
QY 301 GTACATCAACAATGAAATTCGGGGCTAGAGATCTGTGTAACCGTGCATTAACGACTGTG 360  
Db 301 GTACATCAACAATGAAATTCGGGGCTAGAGATCTGTGTAACCGTGCATTAACGACTGTG 360  
QY 361 ATTGACCTCTTTTCTTGGCAAATGTTTCCAGCGGATGTTGAGTTTGGACCTTCG 420  
Db 361 ATTGACCTCTTTTCTTGGCAAATGTTTCCAGCGGATGTTGAGTTTGGACCTTCG 420  
QY 421 TGGCGCATTTCAACAGTTGAGCGCTGCAAAAAGCGGACCTCCGCAATGCGCAATAGCCCC 480  
Db 421 TGGCGCATTTCAACAGTTGAGCGCTGCAAAAAGCGGACCTCCGCAATGCGCAATAGCCCC 480  
QY 481 GATTGATCTCACTGACCAATAGTCAAGTGGCGGTGTGATGTAATTTGGCTGGAGAAATTTG 540  
Db 481 GATTGATCTCACTGACCAATAGTCAAGTGGCGGTGTGATGTAATTTGGCTGGAGAAATTTG 540  
QY 541 CGAATATTTGCTTTCTTCAAGTACGTCAACAGTGAATCCAAAGTGGCAAGTTGAGCGGT 600  
Db 541 CGAATATTTGCTTTCTTCAAGTACGTCAACAGTGAATCCAAAGTGGCAAGTTGAGCGGT 600  
QY 601 GACCTGCGGATGGCGCTGATCTATAGCAATGAGATACAGCTTGAATACGATCACAT 660  
Db 601 GACCTGCGGATGGCGCTGATCTATAGCAATGAGATACAGCTTGAATACGATCACAT 660  
QY 661 CTTCACCAACATCGGTGTGAGAGAGATGCCGGTCAACGTTGATTCATGTTGGGCA 720  
Db 661 CTTCACCAACATCGGTGTGAGAGAGATGCCGGTCAACGTTGATTCATGTTGGGCA 720  
QY 721 GTTGGACACCACTTCTCCAACTGTGTGAGTTGACCGTTTGAATCCGTTCCATTCAAGC 780  
Db 721 GTTGGACACCACTTCTCCAACTGTGTGAGTTGACCGTTTGAATCCGTTCCATTCAAGC 780  
QY 781 TGGTGCTACCCCGCTGAGGTTGCCGAGAAAATCTGGAAGATGGAAGCAATGCCCTGC 840  
Db 781 TGGTGCTACCCCGCTGAGGTTGCCGAGAAAATCTGGAAGATGGAAGCAATGCCCTGC 840  
QY 841 GTCTTATGTTTCCCTGTGCTGTGCTTGGCTGGGCAATGATGGGTGGCTGTGTGT 900  
Db 841 GTCTTATGTTTCCCTGTGCTGTGCTTGGCTGGGCAATGATGGGTGGCTGTGTGT 900  
QY 901 GCTGTTGGGTGAGTGAAGAGATTTCCCTAATTTGCTTTATTAACCGCGTTACAGATCAT 960  
Db 901 GCTGTTGGGTGAGTGAAGAGATTTCCCTAATTTGCTTTATTAACCGCGTTACAGATCAT 960  
QY 961 TGGCAGCAGCTCAATTTTGGGAAAAGAGGTTTGGCTTCTTCCAAAATGTTGTG 1020  
Db 961 TGGCAGCAGCTCAATTTTGGGAAAAGAGGTTTGGCTTCTTCCAAAATGTTGTG 1020  
QY 1021 TGGTTTATTTGCAACGCTGCTGATGATTTGCTTATTTTGGCTTGGCAATTTGGTCT 1080  
Db 1021 TGGTTTATTTGCAACGCTGCTGATGATTTGCTTATTTTGGCTTGGCAATTTGGTCT 1080

QY 1081 TGAATCAAAACGAGCCAGATCATCGACTGTGAATTTGTGTGCTGTTGGAGGTTTGC 1140  
Db 1081 TGAATCAAAACGAGCCAGATCATCGACTGTGAATTTGTGTGCTGTTGGAGGTTTGC 1140  
QY 1141 ACTTGTGAATCTCTGCAGAGACGGGATACGGGGCTTCGGGTGACAGCAATGTGACGATT 1200  
Db 1141 ACTTGTGAATCTCTGCAGAGACGGGATACGGGGCTTCGGGTGACAGCAATGTGACGATT 1200  
QY 1201 TTTTGAACAACCTCCGTTTACCGCGGATTTGTGTGCTGGCGGTGGGTTGGGATTCACCT 1260  
Db 1201 TTTTGAACAACCTCCGTTTACCGCGGATTTGTGTGCTGGCGGTGGGTTGGGATTCACCT 1260  
QY 1261 TTTGAAATCTTGATGATGATGTTGCTGCTGATGAGAGTCCGCTGAGCACTAATTTATTC 1320  
Db 1261 TTTGAAATCTTGATGATGATGTTGCTGCTGATGAGAGTCCGCTGAGCACTAATTTATTC 1320  
QY 1321 GTCTACATTCGCGCGCATTTATGCTGTGTGAGGTGACCGAGCGGCTTTGCAATGAGGTTG 1380  
Db 1321 GTCTACATTCGCGCGCATTTATGCTGTGTGAGGTGACCGAGCGGCTTTGCAATGAGGTTG 1380  
QY 1381 TTACGCGAGTGTCTTCGAGTATTTAGGGGGCTTACCTGCGCTGATGAGGTTTTCGCTT 1440  
Db 1381 TTACGCGAGTGTCTTCGAGTATTTAGGGGGCTTACCTGCGCTGATGAGGTTTTCGCTT 1440  
QY 1441 TTATTAACCTTCGTTGTTTATTTAGGCCCCGCTCTGCGCTGAGATTTGCTGCAACAGC 1500  
Db 1441 TTATTAACCTTCGTTGTTTATTTAGGCCCCGCTCTGCGCTGAGATTTGCTGCAACAGC 1500  
QY 1501 AGTTGTTTCACTGTGTGTTTGTGCTTGGCCGCTGATTTCTTGAATTCACCGTTGATTGCGC 1560  
Db 1501 AGTTGTTTCACTGTGTGTTTGTGCTTGGCCGCTGATTTCTTGAATTCACCGTTGATTGCGC 1560  
QY 1561 GATTGCGGAGATCAACCAATGCTTCAGAGCTTGAAGTTTACCGGGAATGTAAGCGCAC 1620  
Db 1561 GATTGCGGAGATCAACCAATGCTTCAGAGCTTGAAGTTTACCGGGAATGTAAGCGCAC 1620  
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QY 1681 ATCACTTGGCGCTGGGCTGTTTGGGTGATGATTTGCCGAGGCTACGTCGTCAAC 1740  
Db 1681 ATCACTTGGCGCTGGGCTGTTTGGGTGATGATTTGCCGAGGCTACGTCGTCAAC 1740  
QY 1741 ACGCTCAACCCATACCGTGCATTTTACCAAGGGGAATGAGTTCTCTTCCAGAGGAAAGC 1800  
Db 1741 ACGCTCAACCCATACCGTGCATTTTACCAAGGGGAATGAGTTCTCTTCCAGAGGAAAGC 1800  
QY 1801 TGAACAGATCAGCGCGGAGAGAAAAGCTCCAAAGACTAATCAAGATTCGGTAATA 1860  
Db 1801 TGAACAGATCAGCGCGGAGAGAAAAGCTCCAAAGACTAATCAAGATTCGGTAATA 1860  
QY 1861 AAGGTAAATTCAACTGCTTTAGGCGCTTTCCTTAAATAGGTGAAATATCGGTTGGA 1920  
Db 1861 AAGGTAAATTCAACTGCTTTAGGCGCTTTCCTTAAATAGGTGAAATATCGGTTGGA 1920  
QY 1921 TCGCTTTTAAACACTAGAGAGATTCCTTGCAGGCAAAATCAAGCACTCGTCCACCC 1980  
Db 1921 TCGCTTTTAAACACTAGAGAGATTCCTTGCAGGCAAAATCAAGCACTCGTCCACCC 1980  
QY 1981 CAGATATCCTTCAACGCTGTGGAAGAGAAAAGCAGCGGAGTCCGAGATTTGTTCCA 2040  
Db 1981 CAGATATCCTTCAACGCTGTGGAAGAGAAAAGCAGCGGAGTCCGAGATTTGTTCCA 2040  
QY 2041 CCTATTCTAAGGACTTCTTGAAGGGGTCACTTTGATGTCATGCTGGGTTGAACCTC 2100  
Db 2041 CCTATTCTAAGGACTTCTTGAAGGGGTCACTTTGATGTCATGCTGGGTTGAACCTC 2100  
QY 2101 AGGCGCTGGGTTACACCAAGGTGCTTCTGAACACAGAGAGTCAAGCCAAAGAGCTTA 2160  
Db 2101 AGGCGCTGGGTTACACCAAGGTGCTTCTGAACACAGAGAGTCAAGCCAAAGAGCTTA 2160  
QY 2161 CAAAGCGAGCTGTTAAGGACCAAGTAAAGGCTGCTGCTAAGAAAAGCAAGCAAGAGA 2220

Db 2161 CAAAGCGACTCGTAGGCAACAGCTGAGGAGGCTGCTGCTAAGAAAAGCCAGAGAGA 2220  
Qy 2221 CCACATAGAAAGACTACTAAAAAGCAACCGCAAGAAAGACCAAGAGAGCTTTAAGCG 2280  
Db 2221 CCACATAGAAAGACTACTAAAAAGCAACCGCAAGAAAGACCAAGAGAGCTTTAAGCG 2280  
Qy 2281 GATCTTATATGATGATTCGAAATGCTTTGATGTTGTTGCTAACCGCTGCGCATGATA 2340  
Db 2281 GATCTTATATGATGATTCGAAATGCTTTGATGTTGTTGCTAACCGCTGCGCATGATA 2340  
Qy 2341 TGACTGTCCACCCAGATGTGTGCTATACATCTCCCCAGCCGCGTGGCTGTCAAG 2400  
Db 2341 TGACTGTCCACCCAGATGTGTGCTATACATCTCCCCAGCCGCGTGGCTGTCAAG 2400  
Qy 2401 GCGTTTCCCGCTGCTGAGAACACATCGTGAATGTTGGGTGCGATGCGCTGAACTGTAG 2460  
Db 2401 GCGTTTCCCGCTGCTGAGAACACATCGTGAATGTTGGGTGCGATGCGCTGAACTGTAG 2460  
Qy 2461 ATGTTGACCCGGAACCATTTGGAACAGATACGGGTGTTTGTGCTGACCTGTTGCTCA 2520  
Db 2461 ATGTTGACCCGGAACCATTTGGAACAGATACGGGTGTTTGTGCTGACCTGTTGCTCA 2520  
Qy 2521 CTGCAAGGACATATAGAGCTTCTACAGAGGCTTTTCAAGCAACGCTGAGCTCTT 2580  
Db 2521 CTGCAAGGACATATAGAGCTTCTACAGAGGCTTTTCAAGCAACGCTGAGCTCTT 2580  
Qy 2581 TCCACGATTTGATTTGATCTCCGCTGTATCAACACCGATGTGTGATGCTTCCGGAAG 2640  
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Qy 2701 TGCAGACATATACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760  
Db 2701 TGCAGACATATACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760  
Qy 2761 AGATGGTTCCTCTCCACATTCCTCCCTGATCTGTTCCGCTGAGCTGC 2817  
Db 2761 AGATGGTTCCTCTCCACATTCCTCCCTGATCTGTTCCGCTGAGCTGC 2817

RESULT 4  
US-09-783-388-1  
; Sequence 1, Application US/09783388  
; Patent No. US20020168731A1  
; GENERAL INFORMATION:  
; APPLICANT: Ziegler, Petra  
; APPLICANT: Eggeling, Lothar  
; APPLICANT: Sahm, Hermann  
; APPLICANT: Thierbach, Georg  
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND  
; TITLE OF INVENTION: ENZYMATIC PRODUCTION OF L-THREONINE USING CORYNEFORM BACTERIA  
; FILE REFERENCE: 21123/277066  
; CURRENT APPLICATION NUMBER: US/09/783,388  
; CURRENT FILING DATE: 2001-02-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 2817  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum ATCC14752  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (398)..(1864)  
US-09-783-388-1

Query Match 100.0%; Score 2817; DB 9; Length 2817;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAATTAATCCCTCAGCACTGGGACATTCGAAACACCGTTCAATTCGAAACATCG 60  
Db 1 AATGAATTAATCCCTCAGCACTGGGACATTCGAAACACCGTTCAATTCGAAACATCG 60  
Qy 61 AGCCAGGGAAGAAAGAGCCCTTAAGCCCGCTGTATTAATGAGAGCTCTTTGAGAGC 120  
Db 61 AGCCAGGGAAGAAAGAGCCCTTAAGCCCGCTGTATTAATGAGAGCTCTTTGAGAGC 120  
Qy 121 TCAAGCAAAAAGGAGGCAATTTTCAATTAAGAAATACCCCTTTGACCTGCTGTATGAGC 180  
Db 121 TCAAGCAAAAAGGAGGCAATTTTCAATTAAGAAATACCCCTTTGACCTGCTGTATGAGC 180  
Qy 181 TGAAGAGAGAGCTGAAGCTCCTCAACCTACGATTAAGAGTGGCTGCTGCAATTCG 240  
Db 181 TGAAGAGAGAGCTGAAGCTCCTCAACCTACGATTAAGAGTGGCTGCTGCAATTCG 240  
Qy 241 CCACTCCAGCACCGCAGATGCTGATGATCAACACTACGAAATACGATCTTAGCGTATGT 300  
Db 241 CCACTCCAGCACCGCAGATGCTGATGATCAACACTACGAAATACGATCTTAGCGTATGT 300  
Qy 301 GTACATCAATGGAATTCGGGCTAGAGTATCTGTGTAACCGTCAATAAGACCTGTG 360  
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Qy 361 AATGGAATCTTTTCTCCGCAAAATGTTTCCAGCGAGATGTTGAGTTTGGACACCTTCG 420  
Db 361 AATGGAATCTTTTCTCCGCAAAATGTTTCCAGCGAGATGTTGAGTTTGGACACCTTCG 420  
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Db 601 GACCTCTGCTATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
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Db 661 CTTGACCAACATCGGTGCTGAGAGAGATGCGGTCAACGCTTCAATGTTGAGGCA 720  
Qy 721 GTTGACACCACTTCTCAAACTGTCTGAGGTTGACCGTGTGATCGTTCAATTCAGGC 780  
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Db 781 TGGTGTACCCCGCTGAGCTTGGCGAAGAAATTCGACAGAGTTGAGCAATTCGCTGC 840  
Qy 841 GTCTATATGTTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
Db 841 GTCTATATGTTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
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Db 901 GCTGTTGGGTGCTGAGTGCAGAGTTTCCCTAATGCTTTATTAACCGGCTTCAAGATCAT 960  
Qy 961 TGCACAGAGTCAATTTTGGGAAAGAGGTTTGGCTACTTCTTCCAAATATTTGTGG 1020  
Db 961 TGCACAGAGTCAATTTTGGGAAAGAGGTTTGGCTACTTCTTCCAAATATTTGTGG 1020  
Qy 1021 TGGTTTATTTGACAGCTGCTGATGATGCTATTTCTTTGAGCTGCAATTTGTGCT 1080  
Db 1021 TGGTTTATTTGACAGCTGCTGATGATGCTATTTCTTTGAGCTGCAATTTGTGCT 1080



1081 TGAGATCAACCGAGCCAGATCATGCAATGGAATTGTTGTTGTCAGCTTTGAC 1140  
1081 TGAGATCAACCGAGCCAGATCATGCAATGGAATTGTTGTTGTTGAC 1140  
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1861 AAGTGAATCAACCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920  
1861 AAGTGAATCAACCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920  
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2041 CCTATTCTAAGAGATCTTCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTG 2100  
2101 AGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160  
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2161 CAAAGCGAGCTGTAAGGCAACAGCTAAGAGAGAGAGAGAGAGAGAGAGAG 2220

2161 CAAAGCGAGCTGTAAGGCAACAGCTAAGAGAGAGAGAGAGAGAGAGAGAG 2220  
2221 CCCTAAG 2280  
2221 CCCTAAG 2280  
2281 GATCTTATATGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340  
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2341 TGACTGTCAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400  
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2401 GGGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460  
2401 GGGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460  
2461 ATGTTGCAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520  
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2521 CTGCAAGTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580  
2521 CTGCAAGTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580  
2581 TCCAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640  
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2641 TAAACCTCAAGTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700  
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2761 AGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2817  
2761 AGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2817

RESULT 5  
US-09-951-535-1  
; Sequence 1, Application US/09951535  
; Publication No. US20030049802A1  
; GENERAL INFORMATION:  
; APPLICANT: ZIEGLER, PETRA  
; APPLICANT: ZIEGLER, LOTMAR  
; APPLICANT: SAHM, HERMANN  
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND  
; TITLE OF INVENTION: PROCESS FOR THE ENZYMIC PRODUCTION OF L-THREONINE  
; FILE REFERENCE: 21123/28245/MAS  
; CURRENT APPLICATION NUMBER: US/09/951,535  
; CURRENT FILING DATE: 2001-09-14  
; PRIOR APPLICATION NUMBER: 09/431,099  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: DE 199 41 478-5  
; PRIOR FILING DATE: 1999-09-01  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2817  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (398)..(1864)  
; OTHER INFORMATION: LtrE-Gen

US-09-951-535-1

Query Match	100.0%	Score 2817	DB 10	Length 2817
Best Local Similarity	100.0%	Pred. No. 0		
Matches 2817	Conservative 0	Mismatches 0	Indels 0	Gaps 0
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DB 1 AATGAATATATCCCTCACCACCTGGGACATTCAAACACCTTTCAATTCGAAACATCG 60				
QY 61 AGCCAAAGGAAAAAGAAAGCCCTTAAGCCCGGTATTAATGAGAGCTTTGGAGACC 120				
DB 61 AGCCAAAGGAAAAAGAAAGCCCTTAAGCCCGGTATTAATGAGAGCTTTGGAGACC 120				
QY 121 TCAAGCCAAAAAGGGGATTTTCATTAAGAAATATCCCTTTGAACCTGTGTATTGAGC 180				
DB 121 TCAAGCCAAAAAGGGGATTTTCATTAAGAAATATCCCTTTGAACCTGTGTATTGAGC 180				
QY 181 TGGAGAAAGACTTGAACCTGCAACCTAAGCATTAAGAGCTGTGGCTGCCAATTGGC 240				
DB 181 TGGAGAAAGACTTGAACCTGCAACCTAAGCATTAAGAGCTGTGGCTGCCAATTGGC 240				
QY 241 CCACTCCAGCACCCGCAATGCTGATGATCAACACTACGAAATACGATCTTAAGCGTATGT 300				
DB 241 CCACTCCAGCACCCGCAATGCTGATGATCAACACTACGAAATACGATCTTAAGCGTATGT 300				
QY 301 GTACATCAACATGGAATTCGGGGCTAGAGTATCTGTGAAACCGTGCATTAACGACTGTG 360				
DB 301 GTACATCAACATGGAATTCGGGGCTAGAGTATCTGTGAAACCGTGCATTAACGACTGTG 360				
QY 361 ATTGGAATCTTTTCTTTGCAAAATGTTTTCCAGGAGATGTTGAGTTTGGAGACCTTGG 420				
DB 361 ATTGGAATCTTTTCTTTGCAAAATGTTTTCCAGGAGATGTTGAGTTTGGAGACCTTGG 420				
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DB 841 GTCTTAATGCTTCCCTGTTGCTGTGCTGGGCAATGATGGGTGGGCTGTGCTGT 900				
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QY 1021 TGGTTTATATGCAAGCTGCTGCATGCATGATGCTTATTTCTTGGCGTTGCAATTTGATCT 1080				
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DB 1081 TGAATCAAAACGAGCGAGATCATGCAATCTGGAATTTGTTGCTGTGTGCGAGGTTTGA 1140				
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DB 1141 ACTTGTCAATCTCTGAGAGAGGCAATCACGGGCGCTCCGGTGTACAGCAATGCAAGAT 1200				
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DB 1201 TTTTGAAGACCTGCTGTTTACCGCGGCAATTTGCTGCGGTGGGTTTGGGCAATTCAGCT 1260				
QY 1261 TTCTGAATCTTGCATGTCATGTTGCTGCTGCATGAGATCCGCTGACACCTAATTTTC 1320				
DB 1261 TTCTGAATCTTGCATGTCATGTTGCTGCTGCATGAGATCCGCTGACACCTAATTTTC 1320				
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DB 1321 GTCTACATTTGCGCGCATTTATGCTGTGGGTGCTACCGAGCGGCTTGGCAGTGGT 1380				
QY 1381 GTCTACATTTGCGCGCATTTATGCTGTGGGTGCTACCGAGCGGCTTGGCAGTGGT 1440				
DB 1381 GTCTACATTTGCGCGCATTTATGCTGTGGGTGCTACCGAGCGGCTTGGCAGTGGT 1440				
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DB 1441 TTATTAATCTTCTGTTTATTTAATGAGCCCGCTCTGCGCGCTGCAATGCTGCAACAGC 1500				
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DB 1621 CTGGAATGATCAAACTCTATGAGTTTCAACAATTTGCGGTGCTTTAGCACTGCTTC 1680				
QY 1681 ATCACTTCCGCTGCGGTGTTTGGGAGAGATGCGGCAAGCTACGTCGCAAC 1740				
DB 1681 ATCACTTCCGCTGCGGTGTTTGGGAGAGATGCGGCAAGCTACGTCGCAAC 1740				
QY 1741 ACGCTTCAACCATCAACGCTGCAATTTACCAAGGCGAATGATTTCTCTTCCAGAGAGAGC 1800				
DB 1741 ACGCTTCAACCATCAACGCTGCAATTTACCAAGGCGAATGATTTCTCTTCCAGAGAGAGC 1800				
QY 1801 TGAAGCAATCAAGCGCGCGGCAAGAAAGCTCCAAAGCTAATCAAAAGTTGGATATA 1860				
DB 1801 TGAAGCAATCAAGCGCGCGGCAAGAAAGCTCCAAAGCTAATCAAAAGTTGGATATA 1860				
QY 1861 AAGGTAAATCAACCTGCTTGAAGGCTTTGCTTAAATAGCGAATATCGGCTGA 1920				
DB 1861 AAGGTAAATCAACCTGCTTGAAGGCTTTGCTTAAATAGCGAATATCGGCTGA 1920				
QY 1921 TCGCTTTTAAACATCAGAGAGATCTTTCGCGGCAAAATCAAGGACATCTGCTCCAGC 1980				
DB 1921 TCGCTTTTAAACATCAGAGAGATCTTTCGCGGCAAAATCAAGGACATCTGCTCCAGC 1980				
QY 1981 CAGATCCCTTCAAGCTGTGTAAGAGAAACGAGCGGCTGCGGCAAGATTTGTTGCA 2040				
DB 1981 CAGATCCCTTCAAGCTGTGTAAGAGAAACGAGCGGCTGCGGCAAGATTTGTTGCA 2040				
QY 2041 CCTATCTAAGGACTTCTTCAAGCGGCTCACTTTGATGTCATGCTCGGCTTGAACCTTC 2100				
DB 2041 CCTATCTAAGGACTTCTTCAAGCGGCTCACTTTGATGTCATGCTCGGCTTGAACCTTC 2100				

QY 2101 AGGCGCTGCTTACACCAAGGTCGCTTCTGAAACAGAGGAACTCAGCCAAAGAGCTA 2160  
DB 2101 AGGCGCTGCTTACACCAAGGTCGCTTCTGAAACAGAGGAACTCAGCCAAAGAGCTA 2160  
QY 2161 CAAACCGGACTCGTAAAGGCAACGAGCTAAAGAGGCTGCTTAAGAAAGAGCAAGAGAGA 2220  
DB 2161 CAAACCGGACTCGTAAAGGCAACGAGCTAAAGAGGCTGCTTAAGAAAGAGCAAGAGAGA 2220  
QY 2221 CCACCTAAAGAACTCACTAAAGAAAGACCAACGCAAGAGAGCAAAAGAGCTTAAAGCG 2280  
DB 2221 CCACCTAAAGAACTCACTAAAGAAAGACCAACGCAAGAGAGCAAAAGAGCTTAAAGCG 2280  
QY 2281 GATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340  
DB 2281 GATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340  
QY 2341 TGACTGTCCACCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400  
DB 2341 TGACTGTCCACCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400  
QY 2401 GGCCTTCCCGCTTCTGGAACAACATGCTGATGATGATGATGATGATGATGATGATGATGAT 2460  
DB 2401 GGCCTTCCCGCTTCTGGAACAACATGCTGATGATGATGATGATGATGATGATGATGATGAT 2460  
QY 2461 ATGTTGACCCGAGACCACTTGAACAGATGATGATGATGATGATGATGATGATGATGATGAT 2520  
DB 2461 ATGTTGACCCGAGACCACTTGAACAGATGATGATGATGATGATGATGATGATGATGATGAT 2520  
QY 2521 CTGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580  
DB 2521 CTGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580  
QY 2581 TCCACGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640  
DB 2581 TCCACGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640  
QY 2641 TAAACCTCAAGTTCGCGAGAGCGTGAAGCAAGTGGGCGACACGCGTGGCACTGTGGG 2700  
DB 2641 TAAACCTCAAGTTCGCGAGAGCGTGAAGCAAGTGGGCGACACGCGTGGCACTGTGGG 2700  
QY 2701 TGCAGAGCTATCAAGTTCGCGAGAGCGTGAAGCAAGTGGGCGACACGCGTGGCACTGTGGG 2760  
DB 2701 TGCAGAGCTATCAAGTTCGCGAGAGCGTGAAGCAAGTGGGCGACACGCGTGGCACTGTGGG 2760  
QY 2761 AGATCGGTTCTTCTCCACATTCCTTCCCTTCCCTGATCTGTTCGCTCACTGG 2817  
DB 2761 AGATCGGTTCTTCTCCACATTCCTTCCCTTCCCTGATCTGTTCGCTCACTGG 2817

## RESULT 6

US-10-224-574-9  
Sequence 9, Application US/10224574  
Publication No. US20040101837A1  
GENERAL INFORMATION:  
APPLICANT: Forschungszentrum Jlich GmbH; P. Ziegler, L. Eggeling, H. Sahm,  
APPLICANT: P. Peters-Wendisch  
TITLE OF INVENTION: Nucleotide sequences coding for proteins participating in the syn  
TITLE OF INVENTION: L-Serin, improved process for the microbial manufacture of L-ser  
FILE REFERENCE: FZJ-9912-PCT  
CURRENT APPLICATION NUMBER: US/10/224,574  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 9  
LENGTH: 2817  
TYPE: DNA  
ORGANISM: C. glutamicum ATCC 14 752  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (398)..(1867)  
OTHER INFORMATION: thr E (threonin-exportcarrier)  
US-10-224-574-9

Query Match 100.0%; Score 2817; DB 17; Length 2817;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAATATATCCCTCCACCACTGCGACATTTCAACACCGTTTCATTTCCAAACATCG 60  
DB 1 AATGAATATATCCCTCCACCACTGCGACATTTCAACACCGTTTCATTTCCAAACATCG 60  
QY 61 AGCCAAAGGAAAAGAAAGCCCTTAAGCCCGTGTATTAATGAGACTCTTTGAGAGCC 120  
DB 61 AGCCAAAGGAAAAGAAAGCCCTTAAGCCCGTGTATTAATGAGACTCTTTGAGAGCC 120  
QY 121 TCAAGCCAAAAGGGGCAATTTTCATTAAGAAATATACCCCTTTGACTGCTGTATGAGC 180  
DB 121 TCAAGCCAAAAGGGGCAATTTTCATTAAGAAATATACCCCTTTGACTGCTGTATGAGC 180  
QY 181 TGAAGAGAGACTTGAATCTCAACCTAAGCATTAAGAGTGTGCGCTGCGCAATTGGG 240  
DB 181 TGAAGAGAGACTTGAATCTCAACCTAAGCATTAAGAGTGTGCGCTGCGCAATTGGG 240  
QY 241 CCATTCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGATCTTAAAGGATGT 300  
DB 241 CCATTCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGATCTTAAAGGATGT 300  
QY 301 GTACATCAATGGAATTTGGGGCTAGAGTATCTGATGGAACCGTGCATTAACGACTGTG 360  
DB 301 GTACATCAATGGAATTTGGGGCTAGAGTATCTGATGGAACCGTGCATTAACGACTGTG 360  
QY 361 ATGGAATCTTTTCCCTTGGCAAAATGTTTCCAGCGAGATGATGATGATGATGATGATGATGAT 420  
DB 361 ATGGAATCTTTTCCCTTGGCAAAATGTTTCCAGCGAGATGATGATGATGATGATGATGATGAT 420  
QY 421 TGGCCGATTTCAACAGTTGACGCTGCAAAAGCCGCACTCCGCAATGCGCACTAGCCCC 480  
DB 421 TGGCCGATTTCAACAGTTGACGCTGCAAAAGCCGCACTCCGCAATGCGCACTAGCCCC 480  
QY 481 GATTGATCTACGACATATGTAAGTGGCGGCTGTGATTAATTTGGCTCGGAAATTTGG 540  
DB 481 GATTGATCTACGACATATGTAAGTGGCGGCTGTGATTAATTTGGCTCGGAAATTTGG 540  
QY 541 CGATATTTTGTCTTCTTCAAGATACGTCAAAACAGTGAATCCAAAGTGCAGTGGAGCGT 600  
DB 541 CGATATTTTGTCTTCTTCAAGATACGTCAAAACAGTGAATCCAAAGTGCAGTGGAGCGT 600  
QY 601 GACCTCTGGTATGCGCTGTATCAACAGATGATGATGATGATGATGATGATGATGATGATGAT 660  
DB 601 GACCTCTGGTATGCGCTGTATCAACAGATGATGATGATGATGATGATGATGATGATGATGAT 660  
QY 661 CTTCACCAACATGCGGTGAGAGAGAGAGTCCGCTCAACGCTTTCATGTTGGGCA 720  
DB 661 CTTCACCAACATGCGGTGAGAGAGAGAGTCCGCTCAACGCTTTCATGTTGGGCA 720  
QY 721 GTTGAACACCACTTCTCCAACTGTCTAGAGTTGACGTTTGAATCCGTTCCATTAGGC 780  
DB 721 GTTGAACACCACTTCTCCAACTGTCTAGAGTTGACGTTTGAATCCGTTCCATTAGGC 780  
QY 781 TGGTGATCCCGCGCTGAGTTCGCAAAATTTGAGCAGATGGAACCAATCGCCTGG 840  
DB 781 TGGTGATCCCGCGCTGAGTTCGCAAAATTTGAGCAGATGGAACCAATCGCCTGG 840  
QY 841 GTCTATGATTTCCCTGTTGCGTGTGCGTGGCAATGATGATGATGATGATGATGATGATGAT 900  
DB 841 GTCTATGATTTCCCTGTTGCGTGTGCGTGGCAATGATGATGATGATGATGATGATGATGAT 900  
QY 901 GCTGTGTGGTGTGATGAGAGTTCCTTAATGCTTTATTAACGCGTTACAGATCAT 960  
DB 901 GCTGTGTGGTGTGATGAGAGTTCCTTAATGCTTTATTAACGCGTTACAGATCAT 960  
QY 961 TGGCAAGAGCTGATTTTGGGAAAGAGGTTTGGCTACTTCTTCCAAATGTTGTTGG 1020  
DB 961 TGGCAAGAGCTGATTTTGGGAAAGAGGTTTGGCTACTTCTTCCAAATGTTGTTGG 1020

QY 1021 TGGTTTATTCGACGCGCTGCTGATGATGCTTATTCCTTTGGCGTTGCAATTTGCTC 1080  
DB 1021 TGGTTTATTCGACGCGCTGCTGATGATGCTTATTCCTTTGGCGTTGCAATTTGCTC 1080  
QY 1081 TGAATCAACCAAGCGAGATCAATGCGATCTGGAATGTTGTGCTGTTGCAAGTTTAC 1140  
DB 1081 TGAATCAACCAAGCGAGATCAATGCGATCTGGAATGTTGTGCTGTTGCAAGTTTAC 1140  
QY 1141 ACTTGTCATCTCTGAGAGACGGCATCACGGCGCTCCGGTGAACAGCAATGACGATT 1200  
DB 1141 ACTTGTCATCTCTGAGAGACGGCATCACGGCGCTCCGGTGAACAGCAATGACGATT 1200  
QY 1201 TTTTGAACACTCTGTTTACCGCGGCGATTTGCTGCGGTGGGTTTGGGCAATTCAGCT 1260  
DB 1201 TTTTGAACACTCTGTTTACCGCGGCGATTTGCTGCGGTGGGTTTGGGCAATTCAGCT 1260  
QY 1261 TTTGGAATCTTGAGATGATGATGCTGCGCATGAGTCCGCTGACAGCACTTAATTTTC 1320  
DB 1261 TTTGGAATCTTGAGATGATGATGCTGCGCATGAGTCCGCTGACAGCACTTAATTTTC 1320  
QY 1321 GTCTACATTCGCGCGCATTTATCGCTGCGGTGACCGACGGCGCTTTCGAGTGGGTTG 1380  
DB 1321 GTCTACATTCGCGCGCATTTATCGCTGCGGTGACCGACGGCGCTTTCGAGTGGGTTG 1380  
QY 1381 TTTACGCGAGTGTCTCGGTGATTTATGCGGGGCTTACTGCGGTGAGTGGGTTG 1440  
DB 1381 TTTACGCGAGTGTCTCGGTGATTTATGCGGGGCTTACTGCGGTGAGTGGGTTG 1440  
QY 1441 TTATTTACCTCTGCTGTTTATTTAGCGCGGCTCTGCGCTGCGATGCTGCAACAGC 1500  
DB 1441 TTATTTACCTCTGCTGTTTATTTAGCGCGGCTCTGCGCTGCGATGCTGCAACAGC 1500  
QY 1501 AGTTGGTTTCACTGCTGCTGCTGCTGCGGTGATTTGATTTCACTGCTGATTTGCTGC 1560  
DB 1501 AGTTGGTTTCACTGCTGCTGCTGCTGCGGTGATTTGATTTCACTGCTGATTTGCTGC 1560  
QY 1561 GATTCGCGGATCAACCAATGCTTCCAGTGTACCAATTTTACCGGGAATGTAAGCCAC 1620  
DB 1561 GATTCGCGGATCAACCAATGCTTCCAGTGTACCAATTTTACCGGGAATGTAAGCCAC 1620  
QY 1621 CTGGAATGATCAACCACTCATGGGTTTCAACCAATGCGGTGCTTTAGCCATGCTTC 1680  
DB 1621 CTGGAATGATCAACCACTCATGGGTTTCAACCAATGCGGTGCTTTAGCCATGCTTC 1680  
QY 1681 ATCACTTCCGCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
DB 1681 ATCACTTCCGCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
QY 1741 ACGTTTCAACCATACCGTGTATTTACCAAGCGGATGATGCTTCTTCCAGAGGAGC 1800  
DB 1741 ACGTTTCAACCATACCGTGTATTTACCAAGCGGATGATGCTTCTTCCAGAGGAGC 1800  
QY 1801 TGAAGCAATCAAGCGCGGCAAGAAAGTCCAAAGATTAATCAAAAGATTGCTAATA 1860  
DB 1801 TGAAGCAATCAAGCGCGGCAAGAAAGTCCAAAGATTAATCAAAAGATTGCTAATA 1860  
QY 1861 AAGTAAATCAACCTGCTTAAAGGCTCTTTGCTTAAATAGGATTAATGCTGCTGA 1920  
DB 1861 AAGTAAATCAACCTGCTTAAAGGCTCTTTGCTTAAATAGGATTAATGCTGCTGA 1920  
QY 1921 TGGCTTTTAAACACTAGAGAGATCTTGGCGGCAAAATCAAGGACATCTGCTCCACC 1980  
DB 1921 TGGCTTTTAAACACTAGAGAGATCTTGGCGGCAAAATCAAGGACATCTGCTCCACC 1980  
QY 1981 CAGAATCCCTTCAAGCTGTTGAAGAGAAACCGACCGGCTGCGCAGAGATTGTTCCA 2040  
DB 1981 CAGAATCCCTTCAAGCTGTTGAAGAGAAACCGACCGGCTGCGCAGAGATTGTTCCA 2040  
QY 2041 CCTATTCTAAGAGCTTCTTGAAGAGGCTCACTTTGATGCTGCTGCTGCTGCTGCTGCT 2100  
DB 2041 CCTATTCTAAGAGCTTCTTGAAGAGGCTCACTTTGATGCTGCTGCTGCTGCTGCTGCT 2100  
QY 2101 AAGGCTGCTTACCAAGGCTTCTTGAACAGAGAAAGCTACGCAAAAGAGCTA 2160

DB 2101 AAGGCTGCTTACCAAGGCTTCTTGAACAGAGAAAGCTACGCAAAAGAGCTA 2160  
QY 2161 CAAAGCGACTCTTGAAGACCAAGCTTAAGAGAGGCTGCTTAAGAAACAGCAAGAGA 2220  
DB 2161 CAAAGCGACTCTTGAAGACCAAGCTTAAGAGAGGCTGCTTAAGAAACAGCAAGAGA 2220  
QY 2221 CCACTAAGAAACTTAAAGAAACCAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280  
DB 2221 CCACTAAGAAACTTAAAGAAACCAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280  
QY 2281 GATCTTATGATGATGATTTCCATAGCTTTGATGTTGCTTAAACCTGCTCCAGTGA 2340  
DB 2281 GATCTTATGATGATGATTTCCATAGCTTTGATGTTGCTTAAACCTGCTCCAGTGA 2340  
QY 2341 TGACTGTCCACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400  
DB 2341 TGACTGTCCACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400  
QY 2401 GGGTTTCCCGGCTTCTGGAACCAACATGCTGATGATGATGATGATGATGATGATGATG 2460  
DB 2401 GGGTTTCCCGGCTTCTGGAACCAACATGCTGATGATGATGATGATGATGATGATGATG 2460  
QY 2461 ATGTTGACCCGGAACATTTGGAACAGATACGGGTTTGTGCTGCAACCTGCTGCTCA 2520  
DB 2461 ATGTTGACCCGGAACATTTGGAACAGATACGGGTTTGTGCTGCAACCTGCTGCTCA 2520  
QY 2521 CTGCAAGGATTAAGAGGCTTCTACAGAGGCTTTTCAAGCAAGCTGCTGCTCTTT 2580  
DB 2521 CTGCAAGGATTAAGAGGCTTCTACAGAGGCTTTTCAAGCAAGCTGCTGCTCTTT 2580  
QY 2581 TCCAGATTTGATTTATCTCCGCTGTAACACCGATTTGCTGCTGCTGCTGCTGCTGCTG 2640  
DB 2581 TCCAGATTTGATTTATCTCCGCTGTAACACCGATTTGCTGCTGCTGCTGCTGCTGCTG 2640  
QY 2641 TAAACTCAAGTTGCTGAAGCGCTGAGCCAGAGGCGGCAAGGCTGCTGCTGCTGCTG 2700  
DB 2641 TAAACTCAAGTTGCTGAAGCGCTGAGCCAGAGGCGGCAAGGCTGCTGCTGCTGCTG 2700  
QY 2701 TGAAGGATTAAGAGGCTTCTACAGAGGCTTTTCAAGCAAGCTGCTGCTGCTGCTG 2760  
DB 2701 TGAAGGATTAAGAGGCTTCTACAGAGGCTTTTCAAGCAAGCTGCTGCTGCTGCTG 2760  
QY 2761 AGATGCTTCTCTTCTTCAACATTCCTTCCCTGATCTGCTGCTGCTGCTGCTGCTG 2817  
DB 2761 AGATGCTTCTCTTCTTCAACATTCCTTCCCTGATCTGCTGCTGCTGCTGCTGCTG 2817

RESULT 7  
US-09-738-626-1  
; Sequence 1, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIAI, KEIKO  
; APPLICANT: YOKOI, HARUHIRO  
; APPLICANT: TATEISHI, NAOKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738, 626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 7059  
SOFTWARE: Patentin ver. 3.0  
SRO ID NO: 1  
LENGTH: 3309400  
TYPE: DNA  
ORGANISM: Corynebacterium glutamicum  
US-09-738-626-1

Query Match 98.8%; Score 2783.4; DB 9; Length 3309400;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 2796; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 AATGAATTAATCCCTCAACCACTGGGACATTGAAACCGCTTTCATTTCCAAACATCG 60  
Db 2790585 AATGAATTAATCCCTCAACCACTGGGACATTGAAACCGCTTTCATTTCCAAACATCG 2790644  
QY 61 AGCCAGGAGAAAGAAAGCCCTTAAGCCCGCTGTTAATTAATGAGACTCTTTGAGAC 120  
Db 2790645 AGCCAGGAGAAAGAAAGCCCTTAAGCCCGCTGTTAATTAATGAGACTCTTTGAGAC 2790704  
QY 121 TCAGGCCAAAAGGGGCAATTTTCATTAAGAAATATACCCCTTTGACTGCTGTTATTGAGC 180  
Db 2790705 TCAGGCCAAAAGGGGCAATTTTCATTAAGAAATATACCCCTTTGACTGCTGTTATTGAGC 2790764  
QY 181 TGAAGAGAGACTGGAATCTCAACCTTAAGCATTAAGAGAGAGAGAGAGAGAGAGAGAG 240  
Db 2790765 TGAAGAGAGACTGGAATCTCAACCTTAAGCATTAAGAGAGAGAGAGAGAGAGAGAGAG 2790824  
QY 241 CCACTCCAGACCGCAGATCTGATGATCAACAACCTCAAGATAGTATCTTAAGGATATG 300  
Db 2790825 CCACTCCAGACCGCAGATCTGATGATCAACAACCTCAAGATAGTATCTTAAGGATATG 2790884  
QY 301 GTATATCAATATGAAATTCGGGCGTAGAGTATCTGTGAACCGTGCATTAACAGACTGTG 360  
Db 2790885 GTATATCAATATGAAATTCGGGCGTAGAGTATCTGTGAACCGTGCATTAACAGACTGTG 2790944  
QY 361 ATGAGACTCTTTTCCCTGCAAAATGTTTTCAGCGGATGTGATTTGCGACCTGTG 420  
Db 2790945 ATGAGACTCTTTTCCCTGCAAAATGTTTTCAGCGGATGTGATTTGCGACCTGTG 2791004  
QY 421 TGGCCGCAATTCACAGATTGACGCTGCACAAAGCCGCACTCCGCACTGCGCACTAGCCCC 480  
Db 2791005 TGGCCGCAATTCACAGATTGACGCTGCACAAAGCCGCACTCCGCACTGCGCACTAGCCCC 2791064  
QY 481 GATGATCTCACTGACATGATGTAAGTGGCGGTGATGATGATTTGGCTGCGAATTTG 540  
Db 2791065 GATGATCTCACTGACATGATGTAAGTGGCGGTGATGATGATTTGGCTGCGAATTTG 2791124  
QY 541 CGATATTTTGTCTTCTTCAGGTAAGTCACAAAGTGTATACCAAGTGCAGATTTGAGCGGT 600  
Db 2791125 CGATATTTTGTCTTCTTCAGGTAAGTCACAAAGTGTATACCAAGTGCAGATTTGAGCGGT 2791184  
QY 601 GACCTGTGCGTATGACCTGTATATACGATGTGATATACGTTGATATACATACATACAT 660  
Db 2791185 GACCTGTGCGTATGACCTGTATATACGATGTGATATACGTTGATATACATACATACAT 2791244  
QY 661 CTTCCCAACATGCGGTGAGAGAGAGATGCCGCTCAACGTTTCATGTTGAGGCGAA 720  
Db 2791245 CTTCCCAACATGCGGTGAGAGAGAGATGCCGCTCAACGTTTCATGTTGAGGCGAA 2791304  
QY 721 GTTGGACACCACTTCTCCAACTGTCTGAGGTTGACCGTTGATCCGTTCCATTTACAGC 780  
Db 2791305 GTTGGACACCACTTCTCCAACTGTCTGAGGTTGACCGTTGATCCGTTCCATTTACAGC 2791364  
QY 781 TGGTCTACACCCGCTGAGGTGCGGAGAAATTCCTGACGATGAGCAATCCCTTC 840  
Db 2791365 TGGTCTACACCCGCTGAGGTGCGGAGAAATTCCTGACGATGAGCAATCCCTTC 2791424  
QY 841 GTCTATAGTTTCCCTGTTGCGTCTTGGCTGCGCAATGATGGTGGCGCTGTTGCTGT 900  
Db 2791425 GTCTATAGTTTCCCTGTTGCGTCTTGGCTGCGCAATGATGGTGGCGCTGTTGCTGT 2791484  
QY 901 GCTGTGGGTGGTGGATGGAGGTTCCCTAATGCTTTATTAACGGGTTCCAGATCAT 960

Db 2791485 GCTGTGGGTGGTGGATGGAGGTTCCCTAATGCTTTATTAACGGGTTCCAGATCAT 2791544  
QY 961 TGCCACAGACGTCATTTTGGGAGAAAGGTTTGCTTACTTCTTCCAAAATGTTGTTG 1020  
Db 2791545 TGCCACAGACGTCATTTTGGGAGAAAGGTTTGCTTACTTCTTCCAAAATGTTGTTG 2791604  
QY 1021 TGGTTTATGTCAGCGCGCTGCATGATGCTTATTTCTTTGGCGTTGCAATTTGGTCT 1080  
Db 2791605 TGGTTTATGTCAGCGCGCTGCATGATGCTTATTTCTTTGGCGTTGCAATTTGGTCT 2791664  
QY 1081 TGACATCAACCGACCGACATCATCGATCGAATTTGTTGCTGTTGGCAGGTTGAC 1140  
Db 2791665 TGACATCAACCGACCGACATCATCGATCGAATTTGTTGCTGTTGGCAGGTTGAC 2791724  
QY 1141 ACTTGTCATCTCTGACAGAGCGCATCAGCGGCTCCGCTGACAGCAATGACGAT 1200  
Db 2791725 ACTTGTCATCTCTGACAGAGCGCATCAGCGGCTCCGCTGACAGCAATGACGAT 2791784  
QY 1201 TTTTGAACAATCTGTTTACCGCGGCAATTTGCTGCGGTGGGTTTGGGCAATTCAGCT 1260  
Db 2791785 TTTTGAACAATCTGTTTACCGCGGCAATTTGCTGCGGTGGGTTTGGGCAATTCAGCT 2791844  
QY 1261 TTTGAAATCTTGCAATGTCATGTTGCTGTCATGAGTCCGCTGCACACCTAATTTAT 1320  
Db 2791845 TTTGAAATCTTGCAATGTCATGTTGCTGTCATGAGTCCGCTGCACACCTAATTTAT 2791904  
QY 1321 GTCTCAATTTGCCCCGATTTATGCTGTGCGCTGCACGAGCGGCTTGCAGTGGGTTG 1380  
Db 2791905 GTCTCAATTTGCCCCGATTTATGCTGTGCGCTGCACGAGCGGCTTGCAGTGGGTTG 2791964  
QY 1381 TTACGCGAGTGTGCTCCGCTGATTTATGCGGCGCTTACTGCGCTGATGGGTTCTGCTT 1440  
Db 2791965 TTACGCGAGTGTGCTCCGCTGATTTATGCGGCGCTTACTGCGCTGATGGGTTCTGCTT 2792024  
QY 1441 TTATTAATCTTGTGTTTATTTAATTTAGACCCCGCTCTGCGCGTGCATTTCTGCAACAGC 1500  
Db 2792025 TTATTAATCTTGTGTTTATTTAATTTAGACCCCGCTCTGCGCGTGCATTTCTGCAACAGC 2792084  
QY 1501 AGTTGTTTACAGTGTTGTTGCTTCCCGCTGCATTTCTGATTTCCACCGTTGATGTTG 1560  
Db 2792085 AGTTGTTTACAGTGTTGTTGCTTCCCGCTGCATTTCTGATTTCCACCGTTGATGTTG 2792144  
QY 1561 GATTGCGGCAATCAACCAATGCTTCCAGTCTAGAAATTTACCGGGAATGTAAGCGCAC 1620  
Db 2792145 GATTGCGGCAATCAACCAATGCTTCCAGTCTAGAAATTTACCGGGAATGTAAGCGCAC 2792204  
QY 1621 CTTGAATGATCAACAATGAGGTTTCAACCAATTTGCGGTTGCTTTAGCCACTGCTTC 1680  
Db 2792205 CTTGAATGATCAACAATGAGGTTTCAACCAATTTGCGGTTGCTTTAGCCACTGCTTC 2792264  
QY 1681 ATACCTGCGCGTGGCGTGTGTTTGGGTAGTGTGATGCGCGGAGCTACGTCACCC 1740  
Db 2792265 ATACCTGCGCGTGGCGTGTGTTTGGGTAGTGTGATGCGCGGAGCTACGTCACCC 2792324  
QY 1741 AGCGTTCAACCATACCGCTGATTTACCAAGCGAATGAGTTCTCTTCCAGAGGAAC 1800  
Db 2792325 AGCGTTCAACCATACCGCTGATTTACCAAGCGAATGAGTTCTCTTCCAGAGGAAC 2792384  
QY 1801 TGAGCAATCAAGCGCGCGAGAGAAAGTCCAAAGACTAATCAAGATTCGTAATTA 1860  
Db 2792385 TGAGCAATCAAGCGCGCGAGAGAAAGTCCAAAGACTAATCAAGATTCGTAATTA 2792444  
QY 1861 AAGTAAATCAACCTGTTAAGGCTCTTTCGTTAATACGTAATATCGGGTCCA 1920  
Db 2792445 AAGTAAATCAACCTGTTAAGGCTCTTTCGTTAATATCGTAATATCGGGTCCA 2792504  
QY 1921 TCGCTTTTAAACACTCAGAGAGATCTTCCGCGCAAAATCAAGCACTGCTCCACACC 1980  
Db 2792505 TCGCTTTTAAACACTCAGAGAGATCTTCCGCGCAAAATCAAGCACTGCTCCACACC 2792564  
QY 1981 CAGAAATCCCTTACGCTGTTGAAGGAAACCGACGCGGTGCGCGAGATTTGTTGCA 2040





Db 878 CTACTTCTCCAAAATGTTGTGTGTTTATTGTCACGCTGCTGCATGATTCCT 937  
QY 1056 ATTCTTTGGCGTTGCAATTTGGTCTCTTGATGTCAAAACGAGCCAGATGTCATCTCGAA 1115  
Db 938 ATTCTTTGGCGTTGCAATTTGGTCTCTTGATGTCAAAACGAGCCAGATGTCATCTCGAA 997  
QY 1116 TTGTTGTCTGTGTGGCAGTTTGAACATGTCGCAATCTCTGACAGAGCGGCATCAGCGCG 1175  
Db 998 TTGTTGTCTGTGTGGCAGTTTGAACATGTCGCAATCTCTGACAGAGCGGCATCAGCGCG 1057  
QY 1176 CTCGGGTGACAGCAAGTGACGATTTTGAACACATCTCTGTTTACCGGGCGCATTTGTTG 1235  
Db 1058 CTCGGGTGACAGCAAGTGACGATTTTGAACACATCTCTGTTTACCGGGCGCATTTGTTG 1117  
QY 1236 CTGCGCGTGGTTTGGCGCATTAAGCTTTCTGAAATCTTGACATGTCATGTTGCTCGCATG 1295  
Db 1118 CTGCGCGTGGTTTGGCGCATTAAGCTTTCTGAAATCTTGACATGTCATGTTGCTCGCATG 1177  
QY 1296 AGTCGGCTGACAGCAATTAATGCTGTCATATTCGCGCGATTAATGCTGCTGCTGCTCA 1355  
Db 1178 AGTCGGCTGACAGCAATTAATGCTGTCATATTCGCGCGATTAATGCTGCTGCTGCTCA 1237  
QY 1356 CCGCAGCGGCTTTCGACAGTGGTTGTTACGCGAGTGGTCTCGGTGATTAATGCGGGGCG 1415  
Db 1238 CCGCAGCGGCTTTCGACAGTGGTTGTTACGCGAGTGGTCTCGGTGATTAATGCGGGGCG 1297  
QY 1416 TTACTGCGTGAATGGGTTTCTGCGTTTATTAATCTCTGTTGTTTATTAAGCCCGCTCT 1475  
Db 1298 TTACTGCGTGAATGGGTTTCTGCGTTTATTAATCTCTGTTGTTTATTAAGCCCGCTCT 1357  
QY 1476 CTGCGCGTGGATTTGCTGCAACAGCAGTGGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCT 1535  
Db 1358 CTGCGCGTGGATTTGCTGCAACAGCAGTGGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCT 1417  
QY 1536 TCTTGAATTCACCGTTGATTTGTGGCGATTTGCGCGCATCACCAATGCTTCCAGGTCTAG 1595  
Db 1418 TCTTGAATTCACCGTTGATTTGTGGCGATTTGCGCGCATCACCAATGCTTCCAGGTCTAG 1477  
QY 1596 CAATTTAACCGCGGAATGTAGCCACCTTGATGATCAACACATGATGGGTTTTCACCAACA 1655  
Db 1478 CAATTTAACCGCGGAATGTAGCCACCTTGATGATCAACACATGATGGGTTTTCACCAACA 1537  
QY 1656 TTGCGGTGCTTAGGCACTGCTTCAACCTTGGCGCTGGCGGTGTTTGGGTGATGGA 1715  
Db 1538 TTGCGGTGCTTAGGCACTGCTTCAACCTTGGCGCTGGCGGTGTTTGGGTGATGGA 1597  
QY 1716 TTGCGCGAGGCTACGTGTCACACAGCTTCAACCATACGCTGATTTTACCAAGGCGA 1775  
Db 1598 TTGCGCGAGGCTACGTGTCACACAGCTTCAACCATACGCTGATTTTACCAAGGCGA 1657  
QY 1776 ATGAGTTCTCTTCCAGAGGAAGCTGACAGAGATCAGCGCGGACAGAAAAAGCTCAA 1835  
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QY 1836 AGACTTATCAAGATTCGCTAATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1895  
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QY 1896 TAAATGCGTGAATATCGGGTGCATCGCTTTTAAACACTCAGAGGATCTTTGCGGCGC 1955  
Db 1778 TAAATGCGTGAATATCGGGTGCATCGCTTTTAAACACTCAGAGGATCTTTGCGGCGC 1837  
QY 1956 AAAATCAGGACACATGCTCCCAAGATCCCTTACGCTGTTGAAGAGGAAACCGCA 2015  
Db 1838 AAAATCAGGACACATGCTCCCAAGATCCCTTACGCTGTTGAAGAGGAAACCGCA 1897  
QY 2016 GCCGGTG 2022  
Db 1898 GCCGGGG 1904

RESULT 9  
US-09-963-521-3

Sequence 3, Application US/09963521  
; Patent No. US20020146781A1  
; GENERAL INFORMATION:  
; APPLICANT: ZIEGLER, PETRA  
; APPLICANT: EGBELING, LOTMAR  
; APPLICANT: SAM, HERMANN  
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE  
; TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF  
; TITLE OF INVENTION: L-THREONINE USING CORINEFORM BACTERIA  
; FILE REFERENCE: 21123/282413/MAS  
; CURRENT APPLICATION NUMBER: US/09/963,521  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: 09/431,099  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: DE 199 41 478.5  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 1909  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (280)..(1746)  
; OTHER INFORMATION: thre-Gen  
US-09-963-521-3

Query Match 65.2%; Score 1836.6; DB 9; Length 1909;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 156 CCCCTTGAACCTGCTGATTTAGCTGAGGAAAGACTTAACTTCACTTCAACCTTCAACCTTCA 215  
Db 38 CCCCTTGAACCTGCTGATTTAGCTGAGGAAAGACTTAACTTCACTTCAACCTTCAACCTTCA 97  
QY 216 CAAGTCGTTGCGCTCCCAATTCGCGCACTCCAGCAACCGAGATGCTGATGATCAACAC 275  
Db 98 CAAGTCGTTGCGCTCCCAATTCGCGCACTCCAGCAACCGAGATGCTGATGATCAACAC 157  
QY 276 TACGATACGATCTTACGCTATGCTGATCATCAACATGAAATCGGGGCTAGAGTCTG 335  
Db 158 TACGATACGATCTTACGCTATGCTGATCATCAACATGAAATCGGGGCTAGAGTCTG 217  
QY 336 GTGAACCGGCAATTAAGCAACCTGATGGAATGCACTCTTTCTTCTGCAAAATGTTTTCAGC 395  
Db 218 GTGAACCGGCAATTAAGCAACCTGATGGAATGCACTCTTTCTTCTGCAAAATGTTTTCAGC 277  
QY 396 GGATGTTGATTTTGGCACTTCTGCGCGCATTTCAACAGTGAAGCGTGGCGGCGG 455  
Db 278 GGATGTTGATTTTGGCACTTCTGCGCGCATTTCAACAGTGAAGCGTGGCGGCGG 337  
QY 456 CACCTTCGCGCATGCGCACTAGCCCGGATGATCTCACTGACCAATGTCAGTGGCGGCGG 515  
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QY 516 TGATGAATTTGGCTGCGAATTTGGGATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 575  
Db 398 TGATGAATTTGGCTGCGAATTTGGGATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 457  
QY 576 ATACCAAGGTGCAAGTTGAGCGGTGACCTGCTGCTATGAGCTGCTGCTGCTGCTGCTGCTG 635  
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QY 636 ATATACGTTGATACGATACCATCTTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 695  
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QY 696 TCAAGCTGTTGATGTTGCGCAAGTTGGAACCAACCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 755  
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Db 638 ACCGTTGATCCGTTCCATTCAGGCTGAGCGACCCCGCTGAGTTGCGAAGAAATCC 697  
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 Qy 876 CAATGATGAGTGGCGCTGTTGCTGCTGCTGTTGGGTGATGAGTGGCAAGTTTCCCTAATTG 935  
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 Db 1178 AGTCCGCTGACGACCTTATATTCGTCTACATTCGCGCGGATTAAGCTGAGTGGCGTCA 1237  
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 Db 1238 CCGCAGCGGCTTGCAGTGGGTTGTACGCGAGTGTCTCGGTGATTAATGCGGAGGC 1297  
 Qy 1416 TTACTGCGCTGATGAGGTTCTGCGTTTATTAACCTCTTGTGTTTATTTAGGCCCGCT 1475  
 Db 1298 TTACTGCGCTGATGAGGTTCTGCGTTTATTAACCTCTTGTGTTTATTTAGGCCCGCT 1357  
 Qy 1476 CTGCGCTGCGATTCGTCGACAGAGAGTGTTCACAGTGGTGTGCTTGGCGCTGAT 1535  
 Db 1358 CTGCGCTGCGATTCGTCGACAGAGAGTGTTCACAGTGGTGTGCTTGGCGCTGAT 1417  
 Qy 1536 TCTTGATTCACCGTTGATTTGTGGGATTCGCGGATTCACCAATGCTTCCAGGTCTAG 1595  
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 Db 1598 TTGCGCGAGGCTACGTGTCCACACGCTTCAACCCATACCGTGATTTTACCAAGGCGA 1657  
 Qy 1776 ATGAGTTTCTCTTCCAGAGAGAGCTGACAGAAATAGAGCGCGGAGAGAAACGTTCAA 1835  
 Db 1658 ATGAGTTTCTCTTCCAGAGAGAGCTGACAGAAATAGAGCGCGGAGAGAAACGTTCAA 1717  
 Qy 1836 AAGCTATATCAAGATTGCGTATATTAAGTTAAATCAACCTGCTTATGAGCGTCTTGGCT 1895

Db 1718 AAGCTATATCAAGATTGCGTATATTAAGTTAAATCAACCTGCTTATGAGCGCTTTCGCT 1777  
 Qy 1896 TAAATGCTTAAGATTCGAGGTGATCGCTTTAAACAACAACAGAGATTCCTGCGGCG 1955  
 Db 1778 TAAATGCTTAAGATTCGAGGTGATCGCTTTAAACAACAACAGAGATTCCTGCGGCG 1837  
 Qy 1956 AAATACAGGACACTGCTGCCAACCCAGAAATCCCTTACGCTGTTGAAGAGAAACCGCA 2015  
 Db 1838 AAATACAGGACACTGCTGCCAACCCAGAAATCCCTTACGCTGTTGAAGAGAAACCGCA 1897  
 Qy 2016 GCCGCTG 2022  
 Db 1898 GCCGCGG 1904

RESULT 10  
 US-09-834-721-3  
 ; Sequence 3, Application US/09834721  
 ; Patent No. US2002015551A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RIEPING, MECHTHILD  
 ; TITLE OF INVENTION: PROCESS FOR THE PERMENTATIVE PREPARATION OF L-THREONINE  
 ; FILE REFERENCE: 21123/280169/MAS  
 ; CURRENT APPLICATION NUMBER: US/09/834,721  
 ; PRIOR FILING DATE: 2001-04-16  
 ; PRIOR APPLICATION NUMBER: DE 100 26 494.8  
 ; PRIOR FILING DATE: 2000-05-27  
 ; PRIOR APPLICATION NUMBER: DE 101 02 823.7  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 1909  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium glutamicum  
 ; FEATURE:  
 ; OTHER INFORMATION: ATCC13032  
 ; NAME/KEY: CDS  
 ; LOCATION: (280)..(1746)  
 ; OTHER INFORMATION: thre gene  
 ; US-09-834-721-3

Query Match 65.2%; Score 1836.6; DB 9; Length 1909;  
 Best Local Similarity 99.0%; Pred. No. 0;  
 Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 156 CCCCTTTACCTGCTGTTATGAGCTGAGAGAGACTTGAACCTCAACCTAACCATTA 215  
 Db 38 CCCCTTTACCTGCTGTTATGAGCTGAGAGAGACTTGAACCTCAACCTAACCATTA 97  
 Qy 216 CAAGTGGCTGGCTGCCAATTTGCGCACTCCAGACCGCAGATGCTGATGATCAACAG 275  
 Db 98 CAAGTGGCTGGCTGCCAATTTGCGCACTCCAGACCGCAGATGCTGATGATCAACAG 157  
 Qy 276 TAGCAATACGTAATCTTAGCGATGTGTATACATACATGGAATTTGGGGCTAGAGATCTG 335  
 Db 158 TAGCAATACGTAATCTTAGCGATGTGTATACATACATGGAATTTGGGGCTAGAGATCTG 217  
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 Qy 396 GGAATGTAATTTTGGGACCCCTTGTGCGCGGATTTCAACAGTTGACGCTGCAAAAGCGG 455  
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 Db 338 CACCTTCGCGATGCGCACTAGCGCCGATGATGATCTCAACATATGCAAGTGGCGGCTG 397  
 Qy 516 TGATGAATTTGGCTGAGAGATTTGGGATATTTGCTTTCTTCAAGTACGTCAACAGTG 575  
 Db 398 TGATGAATTTGGCTGAGAGATTTGGGATATTTGCTTTCTTCAAGTACGTCAACAGTG 457

QY 576 ATACCAAGTGCAGAGTTGAGCGGAGCTCTGCGTATGCGCTTACTATACGATGCG 635  
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 Db 518 ATATACGTTGAATACGATACGATACGATACGATACGATACGATACGATACGATACG 577  
 QY 696 TCAACGTTGATGATGTTGAGGCAAGTTGAGCAACCACTTCTCCAACTGCTGAGGTTG 755  
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 Db 698 TGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 757  
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 Db 1238 CCGCAAGCGGCTTTCGAGTGGGTTGTTACGCGAGAGTCTCGGATTAATGCGGAGC 1297  
 QY 1416 TTACGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1475  
 Db 1298 TTACGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1357  
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 Db 1358 CTGCGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1417  
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 Db 1418 TCTTGAATTCACCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1477  
 QY 1596 CAATTTACCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1655  
 Db 1478 CAATTTACCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1537

QY 1656 TTGCGGTTGCTTTAGCCACTGCTTCACTGATGCGCGTGGGCTGTTTGGGATGAGA 1715  
 Db 1538 TTGCGGTTGCTTTAGCCACTGCTTCACTGATGCGCGTGGGCTGTTTGGGATGAGA 1597  
 QY 1716 TTGCGCGGAGGCTTACGCTGCTTCACTGATGCGCGTGGGCTGTTTGGGATGAGA 1775  
 Db 1598 TTGCGCGGAGGCTTACGCTGCTTCACTGATGCGCGTGGGCTGTTTGGGATGAGA 1657  
 QY 1776 ATGAGTTCTGCTTCAAGAGAGAGCTGAGAGATGAGAGAGAGAGAGAGAGAGAGAG 1835  
 Db 1658 ATGAGTTCTGCTTCAAGAGAGAGCTGAGAGATGAGAGAGAGAGAGAGAGAGAGAG 1717  
 QY 1836 AGACTATCAAGATTCGTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 1895  
 Db 1718 AGACTATCAAGATTCGTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 1777  
 QY 1896 TAAATAGCGTGAATATGCGGTTGATGCTTTTAAACCTCAGAGAGATCCTTGCAGC 1955  
 Db 1778 TAAATAGCGTGAATATGCGGTTGATGCTTTTAAACCTCAGAGAGATCCTTGCAGC 1837  
 QY 1956 AAATACAGGACCTGCTCCACCCAGATTCCTTACGCTGTTGAAGAGAAACCGCA 2015  
 Db 1838 AAATACAGGACCTGCTCCACCCAGATTCCTTACGCTGTTGAAGAGAAACCGCA 1897  
 QY 2016 GCCGGTG 2022  
 Db 1898 GCCGGG 1904

RESULT 11  
 US-09-783-388-3  
 ; Sequence 3, Application US/09783388  
 ; Patent No. US20020168731A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ziegler, Petra  
 ; APPLICANT: Eggeling, Lothar  
 ; APPLICANT: Sahm, Hermann  
 ; APPLICANT: Thierbach, Georg  
 ; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND  
 ; TITLE OF INVENTION: PROCESS FOR  
 ; FILE REFERENCE: ENZYMATIC PRODUCTION OF L-THREONINE USING CORYNEFORM BACTERIA  
 ; CURRENT APPLICATION NUMBER: US/09/783,388  
 ; CURRENT FILING DATE: 2001-02-15  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: Patentln version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1909  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium glutamicum ATCC13032  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (280)..(1746)  
 US-09-783-388-3

Query Match 65.2%; Score 1836.6; DB 9; Length 1909;  
 Best Local Similarity 99.0%; Pred. No. 0;  
 Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 156 CCCCTTTGACCTGCTGTTATTTGAGTGGAGAGAGACTTGAACCTTCAACGATTA 215  
 Db 38 CCCCTTTGACCTGCTGTTATTTGAGTGGAGAGAGACTTGAACCTTCAACGATTA 97  
 QY 216 CAAGTGGCTGGGCTGCAATTTGGGCTCCTCAGACCGCGAGATGCTGATGATCAACAC 275  
 Db 98 CAAGTGGCTGGGCTGCAATTTGGGCTCCTCAGACCGCGAGATGCTGATGATCAACAC 157  
 QY 276 TACGAATAAGTATCTTACGATGATGATGATGATGATGATGATGATGATGATGATG 335  
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 QY 336 GTGAACCGTGAATTAAGCACTGATGATGATGATGATGATGATGATGATGATGATGATG 395

Db 218 GTGAACCGTGCAATAACGACCTGTGATTGGACTCTTTCTTTCGAAAATGTTTCACG 277  
QY 396 GGATGTTGAGTTTGGACACCTTCTGTGCGCAATTTCAACAGTTGACGTGCAAAAACCG 455  
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QY 456 CACCTCGGCATGCGCATGTGCCCCGATTGATCTCACTGACCAATAGTCAAGTGGCCGGT 515  
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QY 1896 TAAATAGCGTGAATATTCGGGTGATGCTTTTAAACATCAGAGAGATCTTGGCGGCC 1955  
Db 1778 TAAATAGCGTGAATATTCGGGTGATGCTTTTAAACATCAGAGAGATCTTGGCGGCC 1837  
QY 1956 AAATTCACGAGCATCTGCTCCACCCAGAAATCCCTTACGCTGTGTGAAGAGAAAACGCA 2015  
Db 1838 AAATTCACGAGCATCTGCTCCACCCAGAAATCCCTTACGCTGTGTGAAGAGAAAACGCA 1897  
QY 2016 GCCGGTG 2022  
Db 1898 GCCGGTG 1904

RESULT 12  
US-09-951-535-3  
; Sequence 3, Application US/09951535  
; Publication No. US20030049802A1  
; GENERAL INFORMATION:  
; APPLICANT: ZIEGLER, PETRA  
; APPLICANT: EGGELING, LOTHAR  
; APPLICANT: SAHM, HERMANN  
; APPLICANT: THIERBACH, GEORG  
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND  
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE  
; TITLE OF INVENTION: USING CORYNEFORM BACTERIA  
; FILE REFERENCE: 21123/282415/MAS  
; CURRENT APPLICATION NUMBER: US/09/951,535  
; CURRENT FILING DATE: 2001-09-14  
; PRIOR APPLICATION NUMBER: 09/431,099  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: DE 199 41 478.5  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 1909  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (280)..(1746)  
; OTHER INFORMATION: three-Gen  
US-09-951-535-3

Query Match		65.2%	Score 1836.6	DB 10	Length 1909
Best Local Similarity		99.0%	Pred. No. 0		
Matches 1848		Conservative 0	Mismatches 19	Indels 0	Gaps 0
QY	156	CCCCCTTTGACCGTGTGTTATGAGCTGGAAGAGACTTGAACTCTCAACCTTAAGCATTA	215		
DB	38	CCCCCTTTGACCGTGTGTTATGAGCTGGAAGAGACTTGAACTCTCAACCTTAAGCATTA	97		
QY	216	CAAGTGCCTTGGCGTCCCAATTGGCGCACTCCAGACCGGACGATGCTGATGATCAAC	275		
DB	98	CAAGTGCCTTGGCGTCCCAATTGGCGCACTCCAGACCGGACGATGCTGATGATCAAC	157		
QY	276	TACGAATACGATCTTAGCGATGATGATCATCAACAATGGAATGAGGAGCTGATGATG	335		
DB	158	TACGAATACGATCTTAGCGATGATGATCATCAACAATGGAATGAGGAGCTGATGATG	217		
QY	336	GTGAACCGTGCATTAACGACCTGTGATGACTCTTTTCTTGCAAAATGTTTCCAGC	395		
DB	218	GTGAACCGTGCATTAACGACCTGTGATGACTCTTTTCTTGCAAAATGTTTCCAGC	277		
QY	396	GGATGTTGAGTTTGGCCACCTCTGTGGCGGCAATTTCAAGTTGACGCTGCAAAAGCG	455		
DB	278	GGATGTTGAGTTTGGCCACCTCTGTGGCGGCAATTTCAAGTTGACGCTGCAAAAGCG	337		
QY	456	CACCTCCGCAATGCGCACTAGCCCGATGATCTCAACGACATGATCAAGTGGCGGCTG	515		
DB	338	CACCTCCGCAATGCGCACTAGCCCGATGATCTCAACGACATGATCAAGTGGCGGCTG	397		
QY	516	TGATGAATTTGGCTGCGAGAAATGGCGATATTTTGTCTTCTCAGTACGTCAAACAGTG	575		
DB	398	TGATGAATTTGGCTGCGAGAAATGGCGATATTTTGTCTTCTCAGTACGTCAAACAGTG	457		
QY	576	ATACCAAGGTGCAAGTTGAGCGGTGACTCTGTGCGATGAGCTGTACTATACGATGTG	635		
DB	458	ATACCAAGGTGCAAGTTGAGCGGTGACTCTGTGCGATGAGCTGTACTATACGATGTG	517		
QY	636	ATATACGTTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	695		
DB	518	ATATACGTTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	577		
QY	696	TCAACGTGTTTCAATGTTGTGGGCAAGTTGGAACAACCTTCTCCAACTGTCTGAGGTTG	755		
DB	578	TCAACGTGTTTCAATGTTGTGGGCAAGTTGGAACAACCTTCTCCAACTGTCTGAGGTTG	637		
QY	756	ACCGTTGATGCGTTCATTCAGGCTGTGCTCAACCCGCTGAGGTTCCGAGAAAATTC	815		
DB	638	ACCGTTGATGCGTTCATTCAGGCTGTGCTCAACCCGCTGAGGTTCCGAGAAAATTC	697		
QY	816	TGACAGAGTTGAGCAATGCGCTGCGCTTATGTTTCCCTGTTGGGTTGCTGGCTGGG	875		
DB	698	TGACAGAGTTGAGCAATGCGCTGCGCTTATGTTTCCCTGTTGGGTTGCTGGCTGGG	757		
QY	876	CAATGATGAGTGGCGCTGTGCTGTGCTGTGAGGATGAGGAGGTTTCCCTAATG	935		
DB	758	CAATGATGAGTGGCGCTGTGCTGTGCTGTGAGGATGAGGAGGTTTCCCTAATG	817		
QY	936	CTTTTATTAACCGGCTTCAAGATCATTTGCGACGATCTTTTGGGAAAGAGGTTTTC	995		
DB	818	CTTTTATTAACCGGCTTCAAGATCATTTGCGACGATCTTTTGGGAAAGAGGTTTTC	877		
QY	996	CTACTTCTTCCAAATGTTGTGGGTTTATGTCGAGCGGCTGATGATGATGCTT	1055		
DB	878	CTACTTCTTCCAAATGTTGTGGGTTTATGTCGAGCGGCTGATGATGATGCTT	937		
QY	1056	ATTCTTTGGCGTTGCAATTTGCTTGAATCAACCGGACGATGATGATGATGATG	1115		
DB	938	ATTCTTTGGCGTTGCAATTTGCTTGAATCAACCGGACGATGATGATGATGATG	997		
QY	1116	TTGTTGTGCTGTTGAGAGTTTGAACATTTGTCATCTTGAAGACGCGATCAAGGCG	1175		
DB	998	TTGTTGTGCTGTTGAGAGTTTGAACATTTGTCATCTTGAAGACGCGATCAAGGCG	1057		
QY	1176	CTCCGGTGACAGCAAGTGCAGATTTTGAACAACCTCTGTTTACCGGCGCATGTTG	1235		

DB	1058	CTCCGTTGACAGCAAGTGCAGATTTTTCGAAACCTCTGTTTACCGGCGATTTGTTG	1117		
QY	1236	CTGGGTTGGGTTTGGGCAATTCAGCTTTTGAATCTTGCATGTCAATGCTCCGATG	1295		
DB	1118	CTGGGTTGGGTTTGGGCAATTCAGCTTTTGAATCTTGCATGTCAATGCTCCGATG	1177		
QY	1296	AGTCGCTGAGCACTTAAATTCGTACATTTGCCCCGATTAATGCTGTGGTGCATG	1355		
DB	1178	AGTCGCTGAGCACTTAAATTCGTACATTTGCCCCGATTAATGCTGTGGTGCATG	1237		
QY	1356	CCGAGCGGCTTGCAGTGTGTTTGAACGCGAGTGTCTCCGTTGATTAATGAGGAGC	1415		
DB	1238	CCGAGCGGCTTGCAGTGTGTTTGAACGCGAGTGTCTCCGTTGATTAATGAGGAGC	1297		
QY	1416	TTACTGCGCTATGGGTTCTCGGTTTATTAACCTCTTGTGTTTATTAAGCCCGCT	1475		
DB	1298	TTACTGCGCTATGGGTTCTCGGTTTATTAACCTCTTGTGTTTATTAAGCCCGCT	1357		
QY	1476	CTGCGGCTGCGATTTGTCGAACAGCAGTGTGTTTCACTGTGTGTTTGTGCTGAT	1535		
DB	1358	CTGCGGCTGCGATTTGTCGAACAGCAGTGTGTTTCACTGTGTGTTTGTGCTGAT	1417		
QY	1536	TCCTGATTCACCGTTGATTTGTGCGATTTGCGGATCAACCAATGCTTCCAGTCTAG	1595		
DB	1418	TCCTGATTCACCGTTGATTTGTGCGATTTGCGGATCAACCAATGCTTCCAGTCTAG	1477		
QY	1596	CAATTTACCGCGGATGTAAGCCCACTTGAATGATCAACAATCTGATGCTTCCACA	1655		
DB	1478	CAATTTACCGCGGATGTAAGCCCACTTGAATGATCAACAATCTGATGCTTCCACA	1537		
QY	1656	TTGCGGTTGCTTAGCCACTGCTTCACTCTGCGCGTGGCGTGTGTTGGGTGATGGA	1715		
DB	1538	TTGCGGTTGCTTAGCCACTGCTTCACTCTGCGCGTGGCGTGTGTTGGGTGATGGA	1597		
QY	1716	TTGCCCGCAGGCTTACGTCGTCACACGCTTCAACCATACGCTGATTTACCAAGCGA	1775		
DB	1598	TTGCCCGCAGGCTTACGTCGTCACACGCTTCAACCATACGCTGATTTACCAAGCGA	1657		
QY	1776	ATGAGTTTCTCTTCCAGAGGAAAGCTGAGCAATCAAGCGCGCAGAGAAAAGTCCAA	1835		
DB	1658	ATGAGTTTCTCTTCCAGAGGAAAGCTGAGCAATCAAGCGCGCAGAGAAAAGTCCAA	1717		
QY	1836	AGACTAATCAAAAGTTCGATTAATTAAGGTAATTAACCTGATGAGGCTCTTTCGCT	1895		
DB	1718	AGACTAATCAAAAGTTCGATTAATTAAGGTAATTAACCTGATGAGGCTCTTTCGCT	1777		
QY	1896	TAAATAGCTAAGATATCGGATCGATCGCTTTTAAACACTCAGAGAGATCTTCCGCGC	1955		
DB	1778	TAAATAGCTAAGATATCGGATCGATCGCTTTTAAACACTCAGAGAGATCTTCCGCGC	1837		
QY	1956	AAAATACGAGCACTGTCGCCAACCAGAAATCCCTTCAAGCTGTGTAAGAGAAACCGCA	2015		
DB	1838	AAAATACGAGCACTGTCGCCAACCAGAAATCCCTTCAAGCTGTGTAAGAGAAACCGCA	1897		
QY	2016	GCCGCTG 2022			
DB	1898	GCCGCTG 1904			

RESULT 13  
 US-10-224-574-11  
 ; Sequence 11, Application US/10224574  
 ; Publication No. US20040101837A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Forschungszentrum Jlich GmbH, P. Ziegler, L. Eggeling, H. Sahn,  
 ; APPLICANT: P. Peters-Wendisch  
 ; TITLE OF INVENTION: Nucleotide sequences coding for proteins participating in the syn  
 ; TITLE OF INVENTION: L-Series, improved process for the microbial manufacture of L-ser  
 ; FILE REFERENCE: FZJ-9912-PCF  
 ; CURRENT APPLICATION NUMBER: US/10/224, 574  
 ; CURRENT FILING DATE: 2002-08-21

NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 11  
 LENGTH: 1909  
 TYPE: DNA  
 ORGANISM: C. glutamicum ATCC 13 032  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (280)..(1746)  
 OTHER INFORMATION: thr E (Threonine-exportcarrier)  
 US-10-224-574-11

Query Match 65.2%; Score 1836.6; DB 17; Length 1909;  
 Best Local Similarity 99.0%; Pred. No. 0;  
 Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

156 CCCCTTTGACCTGGTGTATTTGAGCTGGAGAGAGACTTGAACCTTCAACCTTACGCATTA 215  
 38 CCCCTTTGACCTGGTGTATTTGAGCTGGAGAGAGACTTGAACCTTCAACCTTACGCATTA 97  
 216 CAAGTGGCTTGGCTGGCCAAATGGCCCACTCCAGCACCGGAGATGCTGATGATCAAC 275  
 98 CAAGTGGCTTGGCTGGCCAAATGGCCCACTCCAGCACCGGAGATGCTGATGATCAAC 157  
 276 TACGAATACGATCTTACGCTATGTATCATCAAAATGGAATTTGGGGCTTAAATCTG 335  
 158 TACGAATACGATCTTACGCTATGTATCATCAAAATGGAATTTGGGGCTTAAATCTG 217  
 336 GTGAACCGTGTATTAAG 395  
 218 GTGAACCGTGTATTAAG 277  
 396 GGATGTTGAGTTTGGAG 455  
 278 GGAATGTTGAGTTTGGAG 337  
 456 CACCTCCGCACTCCGCACTCCGCACTCCGCACTCCGCACTCCGCACTCCGCACTCC 515  
 338 CACCTCCGCACTCCGCACTCCGCACTCCGCACTCCGCACTCCGCACTCCGCACTCC 397  
 516 TGATGAATTTGGCTGGAG 575  
 398 TGATGAATTTGGCTGGAG 457  
 576 ATACCAAGTGTGAATTCGAGCGATGACCTCTGCGATGACCTCTGCTATTAACGATG 635  
 458 ACACCAAGTGTGAATTCGAGCGATGACCTCTGCGATGACCTCTGCTATTAACGATG 517  
 636 ATATCAAGTGTGAATTCGAGCGATGACCTCTGCGATGACCTCTGCTATTAACGATG 695  
 518 ATATCAAGTGTGAATTCGAGCGATGACCTCTGCGATGACCTCTGCTATTAACGATG 577  
 696 TCAAGTGTGTATGATGTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 755  
 578 TCAAGTGTGTATGATGTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 637  
 756 ACCGTTTGAATCCGTTCCATTCAGGCTGAGCTGACCTCCGCTGAGGTTGCGGAGAAAT 815  
 638 ACCGTTTGAATCCGTTCCATTCAGGCTGAGCTGAGCTGACCTCCGCTGAGGTTGCGG 697  
 816 TGGAGAGAGTTGGAG 875  
 698 TGGAGAGAGTTGGAG 757  
 876 CAATGATGGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 935  
 758 CAATGATGGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 817  
 936 CTTTATTAACCGGTTTACGATCATTTGCAACGATCATTTTGGAGAGAGAGAGAGAGAG 995  
 818 CTTTATTAACCGGTTTACGATCATTTGCAACGATCATTTTGGAGAGAGAGAGAGAGAG 877  
 996 CTAATTTCTTCCAAATGTTTGTGTGTTTATTCGACAGCTGCGCATGATGCTT 1055

878 CTAATTTCTTCCAAATGTTTGTGTGTTTATTCGACAGCTGCGCATCATGCTT 937  
 1056 ATTCTTTGGCTTGAATTTGGCTTGAATGAATGAATGAATGAATGAATGAATGAATGA 1115  
 938 ATTCTTTGGCTTGAATTTGGCTTGAATGAATGAATGAATGAATGAATGAATGAATGA 997  
 1116 TTGTGTGCTTGTGGAGAGTTTGAACACTTGTGCAATCTCTGCAAGAGAGAGAGAGAG 1175  
 998 TTGTGTGCTTGTGGAGAGTTTGAACACTTGTGCAATCTCTGCAAGAGAGAGAGAGAG 1057  
 1176 CTCGGTGAACAG 1235  
 1058 CTCGGTGAACAG 1117  
 1236 CTCGGTGGTGTGGAG 1295  
 1118 CTCGGTGGTGTGGAG 1177  
 1296 AGTCCGCTGAG 1355  
 1178 AGTCCGCTGAG 1237  
 1356 CCGGAG 1415  
 1238 CCGGAG 1297  
 1416 TTACTGTGCTGATGAG 1475  
 1298 TTACTGTGCTGATGAG 1357  
 1476 CTGCGGCTGAG 1535  
 1358 CTGCGGCTGAG 1417  
 1536 TCTTGATTCACCGTTGATTTGTGGAGATGCGGAGATGCGGAGATGCGGAGATGCGGAG 1595  
 1418 TCTTGATTCACCGTTGATTTGTGGAGATGCGGAGATGCGGAGATGCGGAGATGCGGAG 1477  
 1596 CAATTTACCGGAG 1655  
 1478 CAATTTACCGGAG 1537  
 1656 TTGCGGTTGCTTGAACCACTGCTTCATCACTTCCGCTGGCGGCTGTTTGGGTGATGA 1715  
 1538 TTGCGGTTGCTTGAACCACTGCTTCATCACTTCCGCTGGCGGCTGTTTGGGTGATGA 1597  
 1716 TTGCGGAG 1775  
 1598 TTGCGGAG 1657  
 1776 ATGATGTTCTCTTCCAG 1835  
 1658 ATGATGTTCTCTTCCAG 1717  
 1836 AGACTAATCAAGATTCGGTAAATTAAGAGTAAATTAAGAGTAAATTAAGAGTAAATTA 1895  
 1718 AGACTAATCAAGATTCGGTAAATTAAGAGTAAATTAAGAGTAAATTAAGAGTAAATTA 1777  
 1896 TAAATGAGTAAATTAAGAGTAAATTAAGAGTAAATTAAGAGTAAATTAAGAGTAAATTA 1955  
 1778 TAAATGAGTAAATTAAGAGTAAATTAAGAGTAAATTAAGAGTAAATTAAGAGTAAATTA 1837  
 1956 AAATACAG 2015  
 1838 AAATACAG 1897  
 2016 GCCGGTG 2022  
 1898 GCCGGTG 1904

RESULT 14

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US-10-627-476-557
; Sequence 557, Application US/10627476
; Publication No. US20040030116A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Mark
; APPLICANT: Krieger, Burkhard
; APPLICANT: Schoder, Hartwig
; APPLICANT: Zeidler, Oskar
; APPLICANT: Haberer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE REFERENCE: BGI-125PCN
; CURRENT APPLICATION NUMBER: US/10/627,476
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 09/602,787
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US/99/60,141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 557
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1567)
; OTHER INFORMATION: KXN00349
US-10-627-476-557
Query Match 55.4%; Score 1561.2; DB 13; Length 1590;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1572; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Db 301 AGTGAAGCTGTCGATGAGTGTGTAATACAGCAGCATGTGATATACAGTTGAATACATAC 360
QY CATCTTCAACCAATCGGTGTGAGAGAGAAATGCCGTCAACGCTTTATGTTGTGGG 717
Db 361 CATCTTCAACCAATCGGTGTGAGAGAGAAATGCCGTCAACGCTTTATGTTGTAGG 420
QY CAAGTTGACACCAACTTCTCCAAACTGTGAGGTGACGTTGATCCGTTCAATCA 777
Db 421 CAAGTTGACACCAACTTCTCCAAACTGTGAGGTGACGTTGATCCGTTCAATCA 480
QY GAGCTGTGCTACCCCGCTGAGAGTTGCCAGAAATTCGACGAGTTGAGACAAATCCC 837
Db 481 GAGCTGTGCTACCCCGCTGAGAGTTGCCAGAAATTCGACGAGTTGAGACAAATCCC 540
QY TGCGCTTATGAGTTTCCCTGTGAGTTGCTTGGCTGGGCAATGATGGGTGGCTGTTC 897
Db 898 TGCGCTTATGAGTTTCCCTGTGAGTTGCTTGGCTGGGCAATGATGGGTGGCTGTTC 897
QY TGCGCTTATGAGTTTCCCTGTGAGTTGCTTGGCTGGGCAATGATGGGTGGCTGTTC 897
Db 541 TGCGCTTATGAGTTTCCCTGTGAGTTGCTTGGCTGGGCAATGATGGGTGGCTGTTC 600
QY 898 TGCGCTTATGAGTTTCCCTGTGAGTTGCTTGGCTGGGCAATGATGGGTGGCTGTTC 957
Db 601 TGCGCTTATGAGTTTCCCTGTGAGTTGCTTGGCTGGGCAATGATGGGTGGCTGTTC 660
QY 958 CATTGCCACGACGTCATTTTGGGAAAGAGAGTTGGCTTCTTCCAAATGTTGT 1017
Db 661 CATTGCCACGACGTCATTTTGGGAAAGAGAGTTGGCTTCTTCCAAATGTTGT 720
QY 1018 TGGTGGTTTATATGACACGCTGCTGATGATGCTTATTTGCGGCTTGCAATTTGG 1077
Db 721 TGGTGGTTTATATGACACGCTGCTGATGATGCTTATTTGCGGCTTGCAATTTGG 780
QY 1078 TCTTGAGATCAAAACGACGATCATGATGATGATGATGATGATGATGATGATGAT 1137
Db 781 TCTTGAGATCAAAACGACGATCATGATGATGATGATGATGATGATGATGATGAT 840
QY 1138 GACCTTGTGATCTCTGAGACGCGATCAACGCGCTCCGCTGACAGCAATGACG 1197
Db 841 GACCTTGTGATCTCTGAGACGCGATCAACGCGCTCCGCTGACAGCAATGACG 900
QY 1198 ATTTTGTGAAACACTCCGTTTACCGGCGCATTTGCTGCGGTGGGTTGGGCAATCA 1257
Db 901 ATTTTGTGAAACACTCCGTTTACCGGCGCATTTGCTGCGGTGGGTTGGGCAATCA 960
QY 1258 GCTTCTGAAATCTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1317
Db 961 GCTTCTGAAATCTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1318 TTGCTTACACTTGGCCCGCATTAATGCTGATGATGATGATGATGATGATGATGAT 1377
Db 1021 TTGCTTACACTTGGCCCGCATTAATGCTGATGATGATGATGATGATGATGATGAT 1080
QY 1378 TTGCTTACACTTGGCCCGCATTAATGCTGATGATGATGATGATGATGATGATGAT 1437
Db 1081 TTGCTTACACTTGGCCCGCATTAATGCTGATGATGATGATGATGATGATGATGAT 1140
QY 1438 GTTTTATACCTTGTGTTTATTTAGGCCCCGCTGCTGCGCTGCGATTTCTGCAAC 1497
Db 1141 GTTTTATACCTTGTGTTTATTTAGGCCCCGCTGCTGCGCTGCGATTTCTGCAAC 1200
QY 1498 AGGAGTTGTTTACAGTGTGTTTGTGCTTGGCCGCTGATTTGATTCACCGTTGAT 1557
Db 1201 AGGAGTTGTTTACAGTGTGTTTGTGCTTGGCCGCTGATTTGATTCACCGTTGAT 1260
QY 1558 GGGGATGGCGGATCAACCAATGATGATGATGATGATGATGATGATGATGATGAT 1617
Db 1261 GGGGATGGCGGATCAACCAATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1618 CACCTTGAATGATCAACCACTGATGATGATGATGATGATGATGATGATGATGAT 1677
Db 1321 CACCTTGAATGATCAACCACTGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1678 TTTCATCACTTGGCGGCTGAGTGTGTTTGGGTGATGATGATGATGATGATGATGAT 1737
Db 1381 TTTCATCACTTGGCGGCTGAGTGTGTTTGGGTGATGATGATGATGATGATGATGAT 1440

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Query 1738 ACCAGCGCTCAACCCATACCGTGCATTTACCAAGGCGAATGATGTTCTTCTTCCAGAGGA 1797  
Db 1441 ACCAGCGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGATGTTCTTCTTCCAGAGGA 1500  
QY 1798 AGCTGACGACAAATCAGGCGCGGACAGAAAACGTCAAAGACTAATCAAGATTCGCTTAA 1857  
Db 1501 AGCTGACGACAAATCAGGCGCGGACAGAAAACGTCAAAGACTAATCAAGATTCGCTTAA 1560  
QY 1858 TAAAGGTAAAGATCAACCTGCTTAAAGCGT 1887  
Db 1561 TAAAGGTAAAGATCAACCTGCTTAAAGCGT 1590

RESULT 15  
US-10-450-055-41  
Sequence 41, Application US/10450055  
Publication No. US20040043953A1  
GENERAL INFORMATION:  
APPLICANT: BASF Aktiengesellschaft  
TITLE OF INVENTION: No. US20040043953A1 genes of *Corynebacterium*  
FILE REFERENCE: 936 2000  
CURRENT APPLICATION NUMBER: US/10/450,055  
CURRENT FILING DATE: 2003-06-10  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn Vers. 2.0  
SEQ ID NO 41  
LENGTH: 1590  
TYPE: DNA  
ORGANISM: *Corynebacterium glutamicum*  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (101)..(1567)  
OTHER INFORMATION: RXS00349  
US-10-450-055-41

Query Match 55.4%; Score 1561.2; DB 13; Length 1590;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 1572; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 298 TGTGTACATCAATGAGAAATCGGGGCTAGAGTATCTGTGTAACCGTGCATTAACGACCT 357  
Db 1 TGTGTACATCAATGAGAAATCGGGGCTAGAGTATCTGTGTAACCGTGCATTAACGACCT 60

QY 358 GTGATTTGACTCTTTTCTTCTTCCAAAATGTTTTCCAGCGGATGTTGAGTTTGGCAACCT 417  
Db 61 GTGATTTGACTCTTTTCTTCTTCCAAAATGTTTTCCAGCGGATGTTGAGTTTGGCAACCT 120

QY 418 TGTGTGCGGCAATTTCAAGAGTTGAGGCTGCAAAAGCCGACCTCCGCACTCCGCACTAGC 477  
Db 121 TGTGTGCGGCAATTTCAAGAGTTGAGGCTGCAAAAGCCGACCTCCGCACTCCGCACTAGC 180

QY 478 CCCGATTGATCTCACTGACCATATGTCAGTGGCCGCTGTGATGAATTTGCTGCGAAT 537  
Db 181 CCCGATTGATCTCACTGACCATATGTCAGTGGCCGCTGTGATGAATTTGCTGCGAAT 240

QY 538 TGGCGAATTTTCTTCTTCTTCCAGTACGTCACCAACATGATCCAAAGTGCAGTTGAGC 597  
Db 241 TGGCGAATTTTCTTCTTCTTCCAGTACGTCACCAACATGATCCAAAGTGCAGTTGAGC 300

QY 598 GGGAGCTCTGCGATGAGCTGTACTATAAGCATGTGATCATACGTTGATATCATGATCAC 657  
Db 301 AGTGACCTCTGCGATGAGCTGTACTATAAGCATGTGATCATACGTTGATATCATGATCAC 360

QY 658 CATCTTCAACCAATCGGTGTGAGAGGAGATGCGGTCAACGTTTCAATGTTGAGG 717  
Db 361 CATCTTCAACCAATCGGTGTGAGAGGAGATGCGGTCAACGTTTCAATGTTGAGG 420

QY 718 CAAAGTGAACCAATCTTCTTCCAAATGATGTGAGTTGACGTTTGAATCCGTTCCATTCA 777  
Db 421 CAAAGTGAACCAATCTTCTTCCAAATGATGTGAGTTGACGTTTGAATCCGTTCCATTCA 480

QY 778 GGGTGTGTGTAACCCGCGCTGAGGTTGCCGAGAAAATTTGAGAGATTTGAGCAATCGCC 837

Db 481 GGGTGTGTGTAACCCGCGCTGAGGTTGCCGAGAAAATTTGAGAGATTTGAGCAATCGCC 540  
QY 838 TGGCTCTTAATGTTTCCCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 897  
Db 541 TGGCTCTTAATGTTTCCCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 600  
QY 898 TGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 957  
Db 601 TGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 660  
QY 958 CATTTGCCAGAGTCATTTTGGGAAAGAGGTTTGGCTTCTTCCAAATGTTG 1017  
Db 661 CATTTGCCAGAGTCATTTTGGGAAAGAGGTTTGGCTTCTTCCAAATGTTG 720  
QY 1018 TGTGTTGTTTATTTGCGACGCTGCTGATGATGTTGTTATTTCTTTGGGTTGCAATTTG 1077  
Db 721 TGTGTTGTTTATTTGCGACGCTGCTGATGATGTTGTTATTTCTTTGGGTTGCAATTTG 780  
QY 1078 TCTTGAGATCAAAACCGACGATCATGCAATGCAATGTTGTTGTTGCGAGTTT 1137  
Db 781 TCTTGAGATCAAAACCGACGATCATGCAATGCAATGTTGTTGTTGCGAGTTT 840  
QY 1138 GACACTGTGCAATCTTCTGCGAGAGCGATCAAGGCGCTCCGTTGACAGAGTGCAG 1197  
Db 841 GACACTGTGCAATCTTCTGCGAGAGCGATCAAGGCGCTCCGTTGACAGAGTGCAG 900  
QY 1198 ATTTTGTGAAACATCTGTTTACCGGCGGATTTGCTGAGCGGTTTGGGATTTCA 1257  
Db 901 ATTTTGTGAAACATCTGTTTACCGGCGGATTTGCTGAGCGGTTTGGGATTTCA 960  
QY 1258 GCTTCTGAAATCTTGCAATGTCATGTTGCTGCAATGAGTGTGCTGAGCACTTAATTA 1317  
Db 961 GCTTCTGAAATCTTGCAATGTCATGTTGCTGCAATGAGTGTGCTGAGCACTTAATTA 1020  
QY 1318 TTTGCTTACATTTGCGCGCATTTATGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1377  
Db 1021 TTTGCTTACATTTGCGCGCATTTATGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1080  
QY 1378 TTTGTTACGCGAGAGTGTGCTGCTGATTTATGCGGAGCTTATCTGCGTGTGATGCTG 1437  
Db 1081 TTTGTTACGCGAGAGTGTGCTGCTGATTTATGCGGAGCTTATCTGCGTGTGATGCTG 1140  
QY 1438 GTTTTATTAACCTTGTGTTTATTTAGGCCCCCTCTGCGCGCTGCGATTCGTCAGAC 1497  
Db 1141 GTTTTATTAACCTTGTGTTTATTTAGGCCCCCTCTGCGCGCTGCGATTCGTCAGAC 1200  
QY 1498 AGCAGTTGTTTCACTGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1557  
Db 1201 AGCAGTTGTTTCACTGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1260  
QY 1558 GCGCATGCGGCAATCAACCAATGCTTCAGAGTCTAGCAATTTACCGCGAAATGTAGCG 1617  
Db 1261 GCGCATGCGGCAATCAACCAATGCTTCAGAGTCTAGCAATTTACCGCGAAATGTAGCG 1320  
QY 1618 CACCTTGAATGATCAAACTCATGAGTTTCAACCAATTTGCGGTTGTTGCGCACTGC 1677  
Db 1321 CACCTTGAATGATCAAACTCATGAGTTTCAACCAATTTGCGGTTGTTGCGCACTGC 1380  
QY 1678 TTTCAATCACTGCGCTGCGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1737  
Db 1381 TTTCAATCACTGCGCTGCGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1440  
QY 1738 ACCAGCTTCAACCCATACCGTGCATTTACAAAGGGAATGATTTCTCTTCCAGAGGA 1797  
Db 1441 ACCAGCTTCAACCCATACCGTGCATTTACAAAGGGAATGATTTCTCTTCCAGAGGA 1500  
QY 1798 AGCTGACGAAATCAGCGCGCGAGAGAAAACGTCAAAGACTAATCAAGATTCGCTTAA 1857  
Db 1501 AGCTGACGAAATCAGCGCGCGAGAGAAAACGTCAAAGACTAATCAAGATTCGCTTAA 1560  
QY 1858 TAAAGGTAAAGATCAACCTGCTTAAAGCGT 1887



Mon Aug 2 07:51:39 2004

us-09-963-521-1.rnpb

Page 21

Db 1561 TAAAGGTAAATCACTGCTAGGCGT 1590

Search completed: July 31, 2004, 10:01:29  
Job time : 1227.59 secs

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OM protein - protein search, using sw model

Run on: July 31, 2004, 04:46:58 ; Search time 39 Seconds

(without alignments)  
647,310 Million cell updates/sec

Title: US-09-963-521-2

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Sequence: 1 MSFATLRGRISTVDAAKAA.....QNGPRQRKPKXTNQRFNKR 489

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/2/1aa/5B COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2432	100.0	489	US-09-431-099-2	Sequence 2, Appli
2	2432	100.0	489	US-09-431-099-4	Sequence 4, Appli
3	143.5	5.9	631	US-09-107-532A-3902	Sequence 3902, Ap
4	143	5.8	254	US-09-134-001C-5543	Sequence 5543, Ap
5	140.5	5.6	256	US-09-252-991A-23462	Sequence 23462, A
6	137	5.6	251	US-09-252-991A-22677	Sequence 22677, A
7	135.5	5.6	270	US-09-328-352-6673	Sequence 6673, Ap
8	134	5.5	274	US-09-134-001C-5279	Sequence 5279, Ap
9	132	5.4	657	US-09-252-991A-27682	Sequence 27682, A
10	129.5	5.3	424	US-09-543-681A-4762	Sequence 4762, Ap
11	128.5	5.3	304	US-09-540-236-3387	Sequence 3387, Ap
12	127.5	5.2	509	US-09-252-991A-32576	Sequence 32576, A
13	127	5.2	704	US-09-252-991A-30631	Sequence 30631, A
14	126.5	5.2	434	US-09-328-352-5070	Sequence 5070, Ap
15	126	5.2	734	US-09-252-991A-33036	Sequence 33036, A
16	125	5.1	638	US-09-252-991A-13036	Sequence 13036, A
17	125	5.1	977	US-09-134-000C-5653	Sequence 5653, Ap
18	124.5	5.1	525	US-09-107-532A-5743	Sequence 5743, Ap
19	124	5.1	474	US-09-489-039A-10432	Sequence 10432, A
20	124	5.1	569	US-09-252-991A-27248	Sequence 27248, A
21	124	5.1	996	US-09-252-991A-27018	Sequence 27018, A
22	123.5	5.1	242	US-09-107-532A-6851	Sequence 6851, Ap
23	123.5	5.1	421	US-09-489-039A-7699	Sequence 7699, Ap
24	123.5	5.1	515	US-09-252-991A-18662	Sequence 18662, A
25	123	5.1	459	US-09-134-000C-5404	Sequence 5404, Ap
26	123	5.1	477	US-09-489-039A-10570	Sequence 10570, A
27	122	5.0	468	US-09-252-991A-27966	Sequence 27966, A

28	121.5	5.0	356	4	US-09-134-000C-4914	Sequence 4914, Ap
29	121.5	5.0	410	4	US-09-328-352-4860	Sequence 4860, Ap
30	121.5	5.0	772	4	US-09-252-991A-30446	Sequence 30446, A
31	120.5	5.0	259	4	US-09-134-000C-6804	Sequence 6804, Ap
32	120.5	5.0	419	4	US-09-252-991A-23245	Sequence 23245, A
33	120.5	5.0	458	4	US-09-328-352-5083	Sequence 5083, Ap
34	120.5	5.0	500	4	US-09-252-991A-25053	Sequence 25053, A
35	120	4.9	444	4	US-09-328-352-6744	Sequence 6744, Ap
36	119.5	4.9	391	4	US-09-489-039A-9791	Sequence 9791, Ap
37	119.5	4.9	443	4	US-09-540-236-3307	Sequence 3307, Ap
38	119	4.9	473	4	US-09-489-039A-14022	Sequence 14022, A
39	119	4.9	494	4	US-09-328-352-7016	Sequence 7016, Ap
40	118.5	4.9	5588	3	US-09-036-987A-6	Sequence 6, Appli
41	118.5	4.9	5588	3	US-09-370-700-6	Sequence 6, Appli
42	118.5	4.9	5588	3	US-09-603-207-6	Sequence 6, Appli
43	118	4.9	438	4	US-09-540-236-2045	Sequence 2045, Ap
44	118	4.9	510	4	US-09-252-991A-29467	Sequence 29467, A
45	118	4.9	1241	4	US-08-714-741-34	Sequence 34, Appli

## ALIGNMENTS

RESULT 1									
US-09-431-099-2									
; Sequence 2, Application US/09431099									
; Patent No. 6410705									
; GENERAL INFORMATION:									
; APPLICANT: Degussa-Höls AG									
; TITLE OF INVENTION: New nucleotide sequences coding for the thre gene and process for									
; FILE REFERENCE: 990079 BT									
; CURRENT APPLICATION NUMBER: US/09/431,099									
; NUMBER OF SEQ ID NOS: 4									
; SOFTWARE: Patentin Ver. 2.1									
; SEQ ID NO 2									
; LENGTH: 489									
; TYPE: PRT									
; ORGANISM: Corynebacterium glutamicum ATCC14752									
US-09-431-099-2									
Query Match									
Best Local Similarity 100.0%; Score 2432; DB 4; Length 489;									
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MSFATLRGRISTVDAAKAA	PPSPPLAPIDLTHSCVAGVMTAARIGDILLSSGTSNSD	60					
DB	1	MSFATLRGRISTVDAAKAA	PPSPPLAPIDLTHSCVAGVMTAARIGDILLSSGTSNSD	60					
QY	61	TKQVRAVTSAYGLYTHVDITLNTTITFTNIGVERKMPNVHVGVKIDTNSKISEVD	120						
DB	61	TKQVRAVTSAYGLYTHVDITLNTTITFTNIGVERKMPNVHVGVKIDTNSKISEVD	120						
QY	121	RIRRSIQAGATPEVEAKILDELOSPASVGFVALLGMMMGAAVAVLLGGGMVSLTA	180						
DB	121	RIRRSIQAGATPEVEAKILDELOSPASVGFVALLGMMMGAAVAVLLGGGMVSLTA	180						
QY	181	FITAFITITATSTLGGKIPPTFQNVVGGFIATLPASIAVSIALQGLIKRPSQIIASGI	240						
DB	181	FITAFITITATSTLGGKIPPTFQNVVGGFIATLPASIAVSIALQGLIKRPSQIIASGI	240						
QY	241	VILLAGLTIVOSIQDITGAPVTASARFPETILLFTGIVAVGLGQISEILLHVMIPAME	300						
DB	241	VILLAGLTIVOSIQDITGAPVTASARFPETILLFTGIVAVGLGQISEILLHVMIPAME	300						
QY	301	SAAPVYSSTFARIIAGGVTAFAVGVCAEWSVLIAGLTMGSAFYLLFVYLGPSV	360						
DB	301	SAAPVYSSTFARIIAGGVTAFAVGVCAEWSVLIAGLTMGSAFYLLFVYLGPSV	360						
QY	361	AAAIATATVGFPGGLARRELLPLIVATAGITPMPLGAIATRGVATINDQTGMFTNI	420						
DB	361	AAAIATATVGFPGGLARRELLPLIVATAGITPMPLGAIATRGVATINDQTGMFTNI	420						

Db 361 AAATAATGVTGGLARRFLIPPLIVAGITPMLGALYRGMATLNDQTMGFNTI 420  
 Oy 421 AVALATASSIAGVVLGEMWIRLRPRPNYPRAFTKANEFSFOEAEQNRQRKPK 480  
 Db 421 AVALATASSIAGVVLGEMWIRLRPRPNYPRAFTKANEFSFOEAEQNRQRKPK 480  
 Oy 481 TMOFRGNKR 489  
 Db 481 TMOFRGNKR 489

## RESULT 2

US-09-431-099-4  
 ; Sequence 4, Application US/09431099  
 ; Patent No. 6410705  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Degussa-Höls AG  
 ; APPLICANT: Forschungszentrum-Jülich GmbH  
 ; TITLE OF INVENTION: New nucleotide sequences coding for the thr gene and process fo  
 ; TITLE OF INVENTION: enzymatic production of L-threonine with corynebacterium bacteria.  
 ; FILE REFERENCE: 990079 BT  
 ; CURRENT APPLICATION NUMBER: US/09/431,099  
 ; CURRENT FILING DATE: 1999-11-01  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 489  
 ; TYPE: PRT  
 ; ORGANISM: Corynebacterium glutamicum ATCC13032  
 ; US-09-431-099-4

Query Match 100.0%; Score 2432; DB 4; Length 489;

Best Local Similarity 100.0%; Pred. No. 4,1e-222; Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MLSPATLGRISTVAAKAPPSPLAPIDLTDHSQVAGVMALARIGDILLSSGTSND 60  
 Db 1 MLSPATLGRISTVAAKAPPSPLAPIDLTDHSQVAGVMALARIGDILLSSGTSND 60  
 Oy 61 TKQVRAVTSAGLYTHVDITLNTITFTNIGVRKMPVNVHVVGKLDTFNSKLSVD 120  
 Db 61 TKQVRAVTSAGLYTHVDITLNTITFTNIGVRKMPVNVHVVGKLDTFNSKLSVD 120  
 Oy 121 RLIRSIQAGATPPEVAEKILDELQSPASYPGFPVALLGMAMGAVAVLLGGQGVSLIA 180  
 Db 121 RLIRSIQAGATPPEVAEKILDELQSPASYPGFPVALLGMAMGAVAVLLGGQGVSLIA 180  
 Oy 181 FTATFTIATTSFLKKGKLPFFQNVVGGFIATLPASIVSIALQFGLTKPSQIIASGI 240  
 Db 181 FTATFTIATTSFLKKGKLPFFQNVVGGFIATLPASIVSIALQFGLTKPSQIIASGI 240  
 Oy 241 VLLAGLTLVQSLQDGTGAPVTASARFETLLFTGGIYAGVGLGIQSEIILHVMLEPME 300  
 Db 241 VLLAGLTLVQSLQDGTGAPVTASARFETLLFTGGIYAGVGLGIQSEIILHVMLEPME 300  
 Oy 301 SAAANYSSTERRIAGVTAAPAVGCAEWSVYIAGLTALMSAEFYLLFVYILGPVS 360  
 Db 301 SAAANYSSTERRIAGVTAAPAVGCAEWSVYIAGLTALMSAEFYLLFVYILGPVS 360  
 Oy 361 AAAIATAVGFTGLARRFLIPPLIVAGITPMLGALYRGMATLNDQTMGFNTI 420  
 Db 361 AAAIATAVGFTGLARRFLIPPLIVAGITPMLGALYRGMATLNDQTMGFNTI 420  
 Oy 421 AVALATASSIAGVVLGEMWIRLRPRPNYPRAFTKANEFSFOEAEQNRQRKPK 480  
 Db 421 AVALATASSIAGVVLGEMWIRLRPRPNYPRAFTKANEFSFOEAEQNRQRKPK 480  
 Oy 481 TMOFRGNKR 489  
 Db 481 TMOFRGNKR 489

## RESULT 3

US-09-107-532A-3902  
 ; Sequence 3902, Application US/09107532A  
 ; Patent No. 6583275  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lynn A Doucette-Stamm and David Bush  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
 ; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
 ; NUMBER OF SEQUENCES: 7310  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
 ; STREET: 100 Beaver Street  
 ; CITY: Waltham  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02354  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: CD-ROM ISO9660  
 ; COMPUTER: PC  
 ; OPERATING SYSTEM: <Unknown>  
 ; SOFTWARE: ASCII  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/107,532A  
 ; FILING DATE: 30-Jun-1998  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/085,598  
 ; FILING DATE: 14 May 1998  
 ; APPLICATION NUMBER: 60/051571  
 ; FILING DATE: July 2, 1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Arinello, Pamela Deneke  
 ; REGISTRATION NUMBER: 40,489  
 ; REFERENCE/DOCKET NUMBER: GTC-012  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (781)893-8277  
 ; TELEFAX: (781)893-8277  
 ; INFORMATION FOR SEQ ID NO: 3902:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 631 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; HYPOTHEetical: YES  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Enterococcus faecium  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (B) LOCATION 1...631  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3902:  
 ; US-09-107-532A-3902

Query Match 5.9%; Score 143.5; DB 4; Length 631;

Best Local Similarity 22.2%; Pred. No. 6,9e-05; Matches 97; Conservative 66; Mismatches 160; Indels 113; Gaps 22;

Oy 92 IGVRRKMPVNVHVVGKLDTFNSKLSVDRLIRSIQAGATPPEVAEKILDEL 142  
 Db 41 VCGEENVS-NVYHCATRLRFLTKDNKKADKEVEQDLEGVITVVEAGMGQVAVNAVNEV 99  
 Oy 143 -----LEQSPAS-----YGFVALLGM-AMMGAVAVLLGGQGVSLIAFIRA 184  
 Db 100 YDVLISKQMKLEDDASSGKRGTEKKGLINSFTIMAAVFPATLGVLAGSLIGVIALCTS 159  
 Oy 185 FTIATTSFLKKGKLPFFQNVVGGFIATLPASIVSIALQFGLTKPSQIIASGIIVLL 244  
 Db 160 INLITLES-----GYIILNAAADAFYFLPLFLAVATAKKTNTD-----RTAMVIAAL 210  
 Oy 245 AGLTIVQSLQDGT-----GAPVTASARFETLLFTGGIYAGVGLGI-----QSEIILH---- 293  
 Db 211 VYPTIVSAVSDSITLRLCMPVIL-ARYNSTYI--PALLAVWLSTYIEKIRKIRSHESIR 267  
 Oy 294 -----WLPAMESAAP--NYSSTERRIAGVTA-----AAFAVGCAEWS 333  
 Db 268 NLTPPICITVWPPIILLVVGFIADYAS--QIIAGYIAVNVFSVLGAVIGGF--WQ 322

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QY 334 SVLIA-----GLTAMMSATYYLLEVVYLGVSAAATATAVGFLGILL-----ARFLLP 383
Db 323 VVITIGLHWGLVPMVMNNISFYGRDITLGPACMTAVAAQGAVALGVFLTKRKKVKSLSIS 382
QY 384 PLIVAIAGIT-EMLPGL-----AIYRGWATLTNDQTLMGFTNIAVALATA 427
Db 383 AITLTLFGITEAAVGVTLTKYKRFYIACICGAIFGVAGGAAG-----ALAVATR 434
QY 428 SLAAGVIGE--MI 440
Db 435 SITSFPIYIGEGFVWL 450

RESULT 4
US-09-134-001C-5543
; Sequence 5543, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5543
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5543

Query Match 5.9%; Score 143; DB 4; Length 254;
Best Local Similarity 22.3%; Pred. No. 2e-05;
Matches 58; Conservative 51; Mismatches 139; Indels 12; Gaps 3;

QY 29 IDLDHSGVAGVMNIAIRIGDITLSSGTSNSDPTKVQVAVTSAYGLYYTHVDITLNTITI 88
Db 6 ITIIDENKVIDIVVLIAGR---ILLEAGAEYRIEDPTNRIRIAHSYGLHDTYSFVSTAIIF 62
QY 89 FTNIGVEKRMVNVHVGVKLDITNFSKLSSEVDRLRSIQAGTTPREVAEKIDELQSPA 148
Db 63 SLNDRSTKYL-----IRIRERTTDEKIALTNLSIRKSSKQLTIDEAKSELLQIKRASL 117
QY 149 SYGEFVALLGAMMGAAVAVLIGGQVSLIAFIATFIATTSFLKGGKGLPTFFQNVYG 208
Db 118 QYSEFLTNLIAFAVAGFLFMFGVASDAMIACLAGIAFLFSFVQKYOIQIKFSEFA 177
QY 209 GFIALTPASIAVSLALQGLBKPSQITASGIVLLIAGLTVQSIQDGTGAPVTASARF 268
Db 178 SAVVISIAIRFTKGIARNDI---ITIASVMPVPGILITNAIRDLIAGELLAGMSRG 233
QY 269 FETLLFTGIVAGVGIQL 288
Db 234 VEALITAFATGAGVAIVLL 253

RESULT 5
US-09-252-991A-23462
; Sequence 23462, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/054,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 3142
; SEQ ID NO 23462
; LENGTH: 526
; TYPE: PR1
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23462

Query Match          5.8%; Score 140.5; DB 4; Length 526;
Best Local Similarity 19.1%; Pred No. 0.0001;
Matches 94, Conservative 78, Mismatches 169, Indels 151, Gaps 19,

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QY	10	RISVVDAAKAP-----PPSPAPIDLDHSGVAVMMLAARIGILSSGTSN	59
Db	63	RAGTLAPRCRGPTFRNCVRCHIDPS-----TTRRPPALAPGRPAHDSRMSADSNYS	116
QY	60	DTKYQVPAVTSANGLYTHVDITLNTITFTNIGVERKMPVNVFHVVKGLDYNFSKLSKV	119
Db	117	QQPPLPAARKSALATSVMLGLTFEFSASMTG-----GLTGTS-----	156
QY	120	DLIRSIQAGATPPEVAEKILDELEQSPASYGFPVALIGWAMMGAVAVLLGGWQVSLI	179
Db	157	-----YDF-----FLAVLSGLMLGLYTHIGFGARTGLS	188
QY	180	APITAPITTIATTSFLKGLPTFFQNVVGFIAITLPAST--AVSLAQSGLEIKPSQIIA	237
Db	189	THLLAHYSVRQOGLLALGVA--RRHGLTVRRRSDDVPKYPVAKATGLDVLLITLVS	245
QY	238	SGIVLV-----LAGLTIVSLODGTGAPAPTASAREPTELLTFGGIYAGVGLIGQISEIL	292
Db	246	GALMTLTFVEFGIAGLTLSAI--AVPAIVLVGSISVWLAVRDAGLAA-----LOOV-	295
QY	293	HVMLPAMESAAPNYSSTFARIITAGVTAAFAVGCYAEV-----SSVITAGLTALMGSA	347
Db	296	-----TPSAPLSTALATLVGSPVSGTLTADVPFGRSARATVAVCVLAFELGS	347
QY	348	FYLLFVYVYIGPVSAAMIAATAVGFTGTLARREPLIYAIAGITPMLPGAIYRQMYA	407
Db	348	LMETLFG--GAQGAIAAGKSDI--SDVMIAGLILIPILVL-----GLNITW----	387
QY	408	TINDQTL---MGFTNIA-----VALATASL-----AAG	433
Db	388	TTNDNALYASGLGFPANITGLSREFLAMNGALGTALALMLYNHFVGLTFLSAIPITGG	447
QY	434	VVIGEWTAERLR	445
Db	448	VITADYLSRRRR	459

RESULT 6  
 US-09-252-991A-22677  
 : Sequence 22677, Application US/09252991A  
 : Patent No. 6551795  
 : GENERAL INFORMATION:  
 : APPLICANT: Marc J. Rubenfield et al.  
 : TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 : FILE REFERENCE: 107196.136  
 : CURRENT APPLICATION NUMBER: US/09/252,991A  
 : PRIORITY FILING DATE: 1999-02-18  
 : PRIOR APPLICATION NUMBER: US 60/074,788  
 : PRIOR FILING DATE: 1998-02-18  
 : PRIOR APPLICATION NUMBER: US 60/094,190  
 : PRIOR FILING DATE: 1998-07-27  
 : NUMBER OF SEQ ID NOS: 33142  
 : SEQ ID NO 22677  
 : LENGTH: 251  
 : TYPE: PRT  
 : ORGANISM: Pseudomonas aeruginosa  
 : US-09-252-991A-22677

Query Match 5.6%; Score 137; DB 4; Length 251;  
 Best Local Similarity 22.7%; Pred. No. 7.2e-05;  
 Matches 68; Conservative 27; Mismatches 134; Indels 70; Gaps 7;

Db 160 AMMGAAVAVLLGGMOVSLIFATFTIATTSFLGKGLPTFQNVVGGFIAT-LPASI 218  
 2 ALVGAAPLIPAGVAEAEALAAAGLGVAAAGFAAGAVGL-----VAAGFAATGFAAGL 55  
 QY 219 AYSIALQFGLKIKPSQIIASGIIVLLAGLTLVSLQDGTGAPVATASARFFETLLFTGGI 278  
 Db 56 AAGFAAG-----AAGLGAAGFAAADPATGILGAAGFAAGLGAAGFAAAGFAAGL 105  
 QY 279 VAGVGLGIGLSEILHWMIPAMESAAPVSTPARIINGVTAAAFNGCAEMSSVILIA 338  
 Db 106 AVGATGFAAGLGAAGFAAAGFAAGFAAGFAAGFAAGFAAGFAAGFAAGFAAGFAV 165  
 QY 339 GLTLMSAPFYLLFVYVGLVPSAAAIAATAVGFTGGLARRELLPPLIVAIAGITPMDG 398  
 Db 166 GLAAGFAAGFAAGFAAGFAAGFAAGFAAGFAAGFAAGFAAGFAAGFAAGFAAG 194  
 QY 399 LAIRGMVATINDQTLMGFTNIAVALATASSLAGVVGEMTARRLRPPFPNPRAPT 457  
 Db 195 -----GFAATVFTAGLAAAFAGLVAG--FAURLSRA--LPASPT 231

RESULT 7  
 US-09-328-352-6673  
 ; Sequence 6673, Application US/09328352  
 ; Patent No. 6562358  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary L. Breton et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
 ; FILE REFERENCE: GTC99-03PA  
 ; CURRENT APPLICATION NUMBER: US/09/328, 352  
 ; CURRENT FILING DATE: 1999-06-04  
 ; NUMBER OF SEQ ID NOS: 8252  
 ; SEQ ID NO 6673  
 ; LENGTH: 470  
 ; TYPE: PRT  
 ; ORGANISM: Acinetobacter baumannii  
 US-09-328-352-6673

Query Match 5.6%; Score 135.5; DB 4; Length 470;  
 Best Local Similarity 21.3%; Pred. No. 0.00026;  
 Matches 93; Conservative 51; Mismatches 141; Indels 151; Gaps 20;

Db 89 FTNIGVERKMPVNVHVGVKLDITNFSKLEVDRLIRSIQAGATPPEVAEKIIDELEQSPA 148  
 Db 119 FTFIGAPKAGP-----TEFAL-----RFTAGLGIGVMMNVVALMTEVAPKIR 163  
 QY 149 SYGFEVALLGMAMMGAAVAVLLG-----GMQVSLIAFTIATTSFLGKGLPTF 202  
 Db 164 STLVAIMFSGYA-IGMTSALLGAWLVKDMGQ-----IMFLA-----GIPDL 206  
 QY 203 FQNVVGGFIATLPASIAVSLAQFGLKIKPSQIIASGIIVLLAGLTVOS-----LDDG 256  
 Db 207 LIPLIMKFP-----IPESLAFIVKSNHSEQ-----AKGIVSKTAPETQANANTQVLINEST 256  
 QY 257 ITGAPVTA--SARFFETLLF----- 274  
 Db 257 TTDAVVRALFOGGRFSTFMFIAPMCLIMVYALGSMVPLKMLQAGVSLGASMLFLPL 316  
 QY 275 -TGGIVAGVGLG-----IQLSEILHWMIPAMESAAPVSTPARIINGVTAAAFNGCAEMSSVILIA 338  
 Db 317 NIGGVGAIGGALADRFLIKPVTIMF-IVGSAA-----LILLGINSPOFIL-- 363  
 QY 329 YAEWSVLIAGLTALMGSAFYVLYGVSAAMIAATAVGFTGGLARRELLPPLIVIA 388  
 Db 364 --YSLINAGATIGSQILLYTFAQFP--TALRSGMWSAGI-----GRICA 409  
 QY 389 IAGITPMLPGIATVGMVATLNDQTLMGF-----TNIAVALATASSLAGVVGEMTARRLRPPFPNPRAPT 442

Db 410 IIG--PVLTG-----TLISFELHQMFLAIPGVIAALAFVWNLKASV 453  
 QY 443 ELRRPPFPNPRAPT 458  
 Db 454 AACTPSTFNQNTLTQ 469

RESULT 8  
 US-09-134-001C-5279  
 ; Sequence 5279, Application US/09134001C  
 ; Patent No. 6380370  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lynn Doucelte-Stamm et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
 ; FILE REFERENCE: GTC-007  
 ; CURRENT APPLICATION NUMBER: US/09/134, 001C  
 ; CURRENT FILING DATE: 1998-08-13  
 ; PRIOR APPLICATION NUMBER: US 60/064,964  
 ; PRIOR FILING DATE: 1997-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/055,779  
 ; PRIOR FILING DATE: 1997-08-14  
 ; NUMBER OF SEQ ID NOS: 5674  
 ; SEQ ID NO 5279  
 ; LENGTH: 274  
 ; TYPE: PRT  
 ; ORGANISM: Staphylococcus epidermidis  
 US-09-134-001C-5279

Query Match 5.5%; Score 134; DB 4; Length 274;  
 Best Local Similarity 22.8%; Pred. No. 0.00016;  
 Matches 60; Conservative 50; Mismatches 123; Indels 30; Gaps 8;

QY 29 IDLDHSCVAGVMMLANIGDILLSSGTSNSDTPKQVRAVTSAYGLTYTHDITINTITI 88  
 Db 26 IETSRALIKDVMIAR---ILLESQAGETRVEDTARIAKLGYPESNFPVT-NTVIE 81  
 QY 89 FT--NIGVERKMPVNVHVGVKLDITNFSKLEVDRLIRSIQAGATPPEVAEKIIDELEQSPA 146  
 Db 82 FVLHNEAVPR-----LYRITRDTNLIKISQANEISQIINGMTLEAKYQLEIYVA 135  
 QY 147 PASYGFEVALLGMAMMGAAVAVL-----LGGWQVSLIAFTIATTSFLGKGL 199  
 Db 136 KRDSLP-----FKGIAAIAIATSFVLYOGGLVDITITVAGLIVLVEIILDRKILH 188  
 QY 200 PTFQNVVGGFIATLPASIAVSLAQFGLKIKPSQIIASGIIVLLAGLTVOSLDDGTG 259  
 Db 189 AQFIDFGLSVIGLISVIGAHFVPSGL---ATIIAAVPIVPGVILITNAIDQLFQG 244  
 QY 260 APVTASARFFETLLFTGGIVAGV 282  
 Db 245 HMLMTTKSLBALVTAFIGAGV 267

RESULT 9  
 US-09-252-991A-27682  
 ; Sequence 27682, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; FILE REFERENCE: 107196,136  
 ; CURRENT APPLICATION NUMBER: US/09/252, 991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 27682  
 ; LENGTH: 657  
 ; TYPE: PRT

ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-27682

Query Match 5.4%; Score 132; DB 4; Length 657;  
Best Local Similarity 22.4%; Pred. No. 0.00091;  
Matches 101; Conservative 67; Mismatches 157; Indels 126; Gaps 25;

```

QY 86 ITFTNGVERKMP-----VNVFHVYKGLDTN-----FSKL-----SEVDRL 122
DB 110 VSIFPS-----RQPEVMILARVLAVMGMIISGTFLLFIITSNPFSSRLPQTRMODDNNLL 164
QY 123 IRSIQAGATPP-----EVAEKIDELQSPASYSYCFPPALLGNMAGCAVA 167
DB 165 LQDGLIVHPPEMLYMGVGSVAFAPALAAVLGRLAAMARWSRPWTWMAAFGLG--IG 222
QY 168 VLLG-----GGM-----QVSLIAFTFTTIIATTSFGKGLPFPQNVVGGF 210
DB 223 IVLGSMWVAYVELGGMGWFMDPVENASFPMLVGTALIHSLAVEKGV--FSS----- 274
QY 211 IATLPASIVASLALQFLEIKPSQIIAS-----GIIVLLAGLTV--QSLQDQITG 259
DB 275 WTVLIAIAAFSLP--LGTFLVRSGLTVSHAFASDPERGVIILAFLLVVGSLTLPLALR 333
QY 260 APVTASARFF-----ETLLFTGGIYAGV-----LGIQSEILHVMIPAMESAAPYSS 309
DB 334 APVKSQVGPALMSREFTLLINLVVAASMLLGLTYPLLDALSGAKLSVGPPEMA 393
QY 310 TPARIIAGVTAAPFAVAGCYAEMSSVLIAGITALMSGAFYLLFVYLGVPYSAALIAATAV 369
DB 394 MELELMA--ALMALAVGVLVRWKDTPSRMLGK-----LTPVLVASAVLAAA 439
QY 370 G-----FTGGLIARFLIPPLIYVLAGITPMLPGAIYRGWATINDQTL---MGFTN 419
DB 440 GSWYFGDFENNAVLA--VELLSAMVY--IAGFDFLDKTR--HKGVLAGASLIFRSYWGQOLAH 496
QY 420 IAVALLATASSLAGVVL--GEMIAAR--LRRP 448
DB 497 LGIAVC-----AIGIVLSQYSACRDLRMSF 522

```

## RESULT 10

US-09-543-681A-4762  
Sequence 4762, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543.681A  
PRIOR FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 4762  
LENGTH: 424  
TYPE: PRT  
ORGANISM: Proteus mirabilis  
US-09-543-681A-4762

Query Match 5.3%; Score 129.5; DB 4; Length 424;  
Best Local Similarity 20.9%; Pred. No. 0.00081;  
Matches 75; Conservative 40; Mismatches 116; Indels 127; Gaps 13;

```

QY 184 AFTIIATTSFLGKKGKLPF-----FQNVGGFIIITLPASTAVSIALQFGEIKPSQI 235
DB 40 ALIKIVTVSFF--WGLATITFALIVFQPIILSKSESVTPATSSIALSLSTGL----- 91
QY 236 IASGIVVLLAGLTVVSLQDGTGAPVTASARF--ETLL-----FTGSIYAGVGLGT 286
DB 92 -----MACGLIITGPLSDAFGRKNVIVIALFCAPFTIILSAMMSMTGILITRALVGL 144
QY 287 QLSLILHVMIPAMESAAPY-----SSTFARIIAGVTAAPFAVAGCYAEM 332

```

DB 145 SLSGVAANVMTYISEEIHFPAYIALSMGLYISGNSIGMSGRVITG-----VLSDYYSW 197

QY 333 S-SVIYIAGLTAMGSAFY-----LFF----- 353

DB 198 RVSIIILGIFALVAAILFWKILPISQHFPAITLKPRNLLITTKIHFPDKGLPLFLFIGGL 257

QY 354 -----VYLGPVSAANAATAVGFTGGLIARFLIPLIYA 388

DB 258 IMGGFVTLFNYIGRLIDAPYSILQTVGLISYLSGTYSAKAGLLTNKYGK--VF 315

QY 389 IAGTPEMLPGAIYRCGYATINDQTMGFNIAVALTPASSLAAGVVLGEMIAARLR 446  
DB 316 IAGVSMILAGILI-----TLFDSLAIIF--IGMLIITTFGFPAHAIVASSVGRRAK 365

## RESULT 11

US-09-540-236-3387  
Sequence 3387, Application US/09540236  
Patent No. 6673910  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATALA  
FILE REFERENCE: 2709.2005-001  
CURRENT APPLICATION NUMBER: US/09/540.236  
PRIOR FILING DATE: 2000-04-04  
NUMBER OF SEQ ID NOS: 3840  
SEQ ID NO 3387  
LENGTH: 304  
TYPE: PRT  
ORGANISM: M. catathalalis  
US-09-540-236-3387

Query Match 5.3%; Score 128.5; DB 4; Length 304;  
Best Local Similarity 18.7%; Pred. No. 0.00061;  
Matches 60; Conservative 60; Mismatches 134; Indels 67; Gaps 8;

```

QY 13 TVDAAKAAPPPSEPLAPIDLTD-----HSQVAGVNNIARIGDILSSGTS 57
DB 8 TIQATKSHF-----MNLADDEMPSLFDPHPSRLNAAQQRITRLICRCLLIMQYGA 61
QY 58 NSDPTKQVRAVTSAYGLYTHVDITNTITITF-----NIGVERMPYNVF 103
DB 62 SVVWVDLTKRLGALGIDGVECGSEFAVATLTLYQRCITTVNNTVHQGINVSLVQIQ 121
QY 104 HVGXKJDTNSKXSEV-----DLRISIQAGATPREVAEKIDELQSP-----ASYGF 152
DB 122 QILISAHENHOANQSHCINTOSHDACTSSVQG-----FPAIVQTVYSNHLVSFPV 171
QY 153 PVALLGNMAMGCAVAVVLLGGQVSLIAFTTIIATTSFLGKKGKLPFPQNVVGGFIA 212
DB 172 GVCASFAVINGATIV-----IALITFASIVAMLRVYLKQHNPNPVVAMITAFYA 224
QY 213 TLPASTAVSIALQFGEIKPSQIIASGIVVLLAGLTVVSLQDGTGAPVTASARFPE 272
DB 225 TLIAALAYFLNLGTNADI-----AVASVLLVPSFPIINALSDIKGYMMNGVGMFPAT 280
QY 273 LFTGVIYAGVGLGIQSLSEILH 293
DB 281 MLTISACVGIWMTIIFLRIPH 301

```

## RESULT 12

US-09-252-991A-32576  
Sequence 32576, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252.991A

```

: CURRENT FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ ID NOS: 33142
: SEQ ID NO 32576
: LENGTH: 509
: TYPE: PRN
: ORGANISM: Pseudomonas aeruginosa
US-03-252-991A-32576

```

Query Match	5.2%;	Score 127.5;	DB 4;	Length 509;
Best Local Similarity	26.7%;	Pred. No. 0.0017;		
Matches 70;	Conservative 31;	Mismatches 86;	Indels 73;	Gaps 13

```

QY      236  IAGIVVLLIAGLITLVLSLDDGITGAPVIA---SARFETLLFTGTGIVAGVIGIGLSEIL 2922
      236  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      255  LAAGVAAAGG---ALEDAGAGGFAAGAAAGLAAGFAAGFAAGLAAGFAAG----- 3022
      255  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      293  HVMLPAMESA--AAPNYSSTARITTAGVTT---AAPVCGCYAEMSVYITAGLTALMGSA 3477
      293  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      303  ---LAAVAAAGLAAGGFAAGFAAALAGIVGFAAFAVGLAAG---LAAGLAAAVFAA 3555
      303  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      348  FYLLFVVYLGVPYSAALIAATAVGTFGGLIAREFLPLIIVLAGITPMLPELATIYRMVYA 4070
      348  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      356  GF---FAAGFAAGLAALLAGLAAGLAAVF-----AGGLA--AGFAA 3933
      356  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      408  TLNDQTLMGFT---NIAVALTASSLAGAVVLGEMIAARLRPR--FNPYRAFTKANEF 4623
      408  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      394  GLAAFAAGLITLVVPFSICIVSVSTL---LCSFSTSLRGTGTPRRERMAFLRRISKASS 4449
      394  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      463  $-----FOREAE 469
      463  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      450  SLHLPARSRSTSLTLPARAE 471
      450  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 13  
US-09-252-991A-30631  
; Sequence 30631, Application US/09252991A

```

1  GENERAL INFORMATION:
2  APPLICANT: Marc J. Rubenfield et al.
3  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
4  TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
5  FILE REFERENCE: 107196.136
6  CURRENT APPLICATION NUMBER: US/09/252,991A
7  CURRENT FILING DATE: 1999-02-18
8  PRIOR APPLICATION NUMBER: US 60/074,788
9  PRIOR FILING DATE: 1998-02-18
10 PRIOR APPLICATION NUMBER: US 60/094,190
11 PRIOR FILING DATE: 1998-07-27
12 NUMBER OF SEQ ID NOS: 33142
13 SEQ ID NO 30631
14 LENGTH: 704
15 TYPE: PR1
16 ORGANISM: Pseudomonas aeruginosa
17 US-09-252-991A-30631

```

Query Match	5.2%	Score 127	DB 4	Length 704
Best Local Similarity	22.1%	Pred. No. 0.003		
Matches 102; Conservative	63	Mismatches 156	Indels 140	Gaps 24

[illegible]

Dh 133 GYLPGL-WLING-----VYLAGAVQDPFWLVEISSRNRGRSIGELVREEMQVAGTIALFCG 185

Qy 185 -----FTIATTSFLGKKGLPFFPNQVNGF--IATIPASIAVIALQFGLKIP---SQ 234

Dh 186 APLIMITIIAVIALIVNALA--DSPGMFTVATITPALEMGVYK---IRPGIGE 239

Qy 235 IIASGIVVLAAGLTVOSLODGTGAPATASAREFETLLPTGVIAG--VGLGIOLSEIL 292

Dh 240 ISIIIGVETLLSGIML-----GGVYAPASPEWAPHFTFSGIQTIMWLIGYCAVS--- 287

Qy 293 HYVLPAMEAANPNVSSTPARIINAGVYAAAFVAGCAEMSIVIAAGTIL-----M 344

Dh 288 --VLPFWILLARPDYUSFLKI-----GITIGLAIGILIVPELMKPDLTQFTDGTGVYK 341

Qy 345 GSAYFLVY-VYIGPVSA--PAIA-----ATAVGFTGGLIARRFLIPLIIVA 388

Dh 342 GSIFPELFTIICGAWSGCFHALISSGTPKLLINREPDARIYGY--GGMIMESFVAIMAMVA 400

Qy 389 IAGITMPLGAIYRGMYATLNDQGLMFTGIIAVALTASS 429

Dh 401 ASVIEP-----GIYFAMNSPRAVVGADVAMVAIVSS 432

```

RESULT 14
US-09-328-352-5070
: Sequence 5070, Application US/09328352
: Patent No. 6562958
: GENERAL INFORMATION:
: APPLICANT: Gary L. Breton et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINIC
: TITLE OF INVENTION: BAUMANNII FOR DIAGNOSIS
: FILE REFERENCE: GTC99-03PA
: CURRENT APPLICATION NUMBER: US/09/328,352
: CURRENT FILING DATE: 1999-06-04
: NUMBER OF SEQ ID NOS: 8252
: SEQ ID NO 5070
: LENGTH: 434
: TYPE: prt
: ORGANISM: Acinetobacter baumannii
US-09-328-352-5070

```

```

; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAIUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5070
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-5070

```

Query Match	5.2%	Score 126.5	DB 4	Length 434
Best Local Similarity	22.8%	Pred. No. 0.0016		
Matches 89	Conservative 50	Mismatches 161	Indels 91	Gaps 19

```

OY      118  ENDRLLRSIQAGATPREVEAKILDELOSPASVSPV---ALLG------AMMGAAV- 168
      |||
Db      17  DVCH--RPVSTNEYLPVPQSAILO-IGHAFNFGATVAPLIMGPNPALIMSGICTIL 73
      |||
OY      169  --LLGGWQWLSIAFIATF--TIIATTSFLGKKKGPTFEFQWVGGFATLPASIASIAL 224
      |||
Db      74  FFLITGRVPSYLGSSFAFIGVAAATGHTTSGGANPMLSTALGGIVA---CGIFVYL-- 128
      |||
OY      225  QFGLEI-----KPSOTIASGVILLAGTLTVQSIQDGTGAP----- 261
      |||
Db      129  -IGFIWLTGTRWIEKMLPVPVYTGAIWMIIGINTLPVTIKGVAGQPFEMMALITVLQMG 187
      |||
OY      262  ---VTSARFEFTLLPTGGIVA-----GVGLG--IOLSEIHWMLPMESGAAPNY 307
      |||
Db      188  SIATVTRGLQRLHLLVGLLIVYIAIATNGLGKGRIDPSQILQASWFOBPFSHPTE 24
      |||
OY      308  SSTFARIIA-----GGVTAAPFVAGCYAEMSSVITAGLTALMGSAFY- -LEVV 35
      |||
Db      248  DTKAILIIVAVALIIVAENLGHKIVAGAMTG-----ENLTPQKGAFAVDGLATY 297
      |||
OY      355  YLGPVSAAIATATAVFTGGLIARRFLPLPLVIAIAGITPMLPGIA-IYRGMYATINDQT 411
      |||
Db      298  LSGSVGAPGM--TTYGENIGVMAWVRVYSTIVFVINGAIFALFLGSPKFAVISTIPSAV 355
      |||
OY      414  LMGFTNIAVALATPASSLAAGVYLGEVIAERLL 444
      |||
Db      356  LTAGSIVYFGLIT---IAGAKI--WIENKK 380

```



RESULT 15

US-09-252-991A-33036

Sequence 33036, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR ETIOLOGICAL AND EPIDEMIOLOGICAL STUDIES

FILE REFERENCE: 107196 136

FILE REFERENCE: 10/196-136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: IIS 60/074 788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094.190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 33036

; LENGTH: 734

TYPE: PRT  
!

ORGANISM:

US-09-252-991A-33036

0  
:  
:  
:  
:

Query Match	5.28;	Score 126;	DB 4;	Length 734;
-------------	-------	------------	-------	-------------

Best Local Similarity 21.9%; Pred. No. 0.004;

Matches 126; Conservative 60; Mismatches 184; Indels 206; Gaps 26;

QY 18 KAAPPSP LAPIDLT DSHQVGV-----MNL AARIGDILLSSGTS-----NSDTKVQV----- 65

Db 257 RAAPPASPREP-SLVERGFAAKGWLFGGNTVLRIGVLLFIQIAFTLRVASERVAAPVE 215

66 -----PAYTSAVCI YETIYIBTEI NMTETEMATCIENKADINUYUW 100

01C				
01B				

\*2 100 PONDINI DISEVNDLINSI QHGH --- IFFEVHENIDDELEQSFASIGFVALLGWA 160

: : : :

263 -----KLHPLISPGALALLVVMICSAIILVLQNA-----MGLAVVA 300

QY 161 MMGAVAVLL---GGQVSLIAFITFT--IIATTSFLGKKGLPTFFQNVGGFIATLP 215

Db 301 ALGGEAPILTSTGSGNHVALFSYFALLNAGIFAIAFWFRWRPL-----NLV-GFVGT-- 352

216 ASIAYSLAQFGLIKPSOIIAS-----GIVVLLAGLTIVOSIO-DGTTGAP 261

```

Db      353  --- EGTGEAWGTPSYTPET.FASTETPET.ALFETMNVYCTET.FBPYTFEADADAECEET 406
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

2022 12 22 15:00

[illegible]

100-443887-100

21 GGVLA-----AFAVGCIAMSSVL-----IAG 339

466 GHASAGRTSLVEICLALGVFTLAIPLGLDARWTSAAWAVEGAGIYWLGLHQRLAR 525

QY 340 LTALM--GSAFYLLFVVLG-----PVSAALAAATAVG----- 370

Db 526 LFALLQGGAALAYINGVRPGETTLLSGSPILGALMIGAALFSEFWOLBRAPAKALADWEP 585

371 -----FTGGT.T.ABREF.T.PDI.TVATAG-----ITBMT.DCI.T.TYBCH.MTMT 400

[illegible]

Search completed: July 31, 2004, 10:02:10  
Job time : 42 secs

Job time : 42 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: July 31, 2004, 10:01:43 ; Search time 110 Seconds

(without alignments)  
2467.009 Million cell updates/sec

Title: US-09-963-521-2

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Egapop 6.0 , Egapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DICALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09963521\_@CGN 1.1.105 @runat.27072004.114907.5657 -MCPU=6 -ICPU=3  
-NO MAP -LARGEDUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:\*  
1: /cgn2\_6/prodata/2/ina/5A.COMB.seq:\*  
2: /cgn2\_6/prodata/2/ina/5B.COMB.seq:\*  
3: /cgn2\_6/prodata/2/ina/6A.COMB.seq:\*  
4: /cgn2\_6/prodata/2/ina/6B.COMB.seq:\*  
5: /cgn2\_6/prodata/2/ina/6C.COMB.seq:\*  
6: /cgn2\_6/prodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	2432	100.0	1909	4	US-09-431-099-3
2	2432	100.0	2817	4	US-09-431-099-1
3	591	24.3	4403765	3	US-09-103-840A-2
4	591	24.3	4411529	3	US-09-103-840A-1
5	190	7.8	9834	4	US-08-956-171E-37
6	163.5	7.0	18436	4	US-08-961-527-87
7	165	6.8	23210	4	US-09-596-003-17
8	146.5	6.0	912	4	US-09-252-991A-6186
9	146.5	6.0	913	4	US-09-252-991A-6186
10	146.5	6.0	1806	4	US-09-252-991A-6445
11	143.5	5.9	1896	4	US-09-107-532A-6023
12	143	5.9	765	4	US-09-134-001C-2706

13	142.5	5.9	1581	4	US-09-252-991A-7755	Sequence 7755, Ap
14	140.5	5.8	1581	4	US-09-252-991A-6891	Sequence 6891, Ap
15	140.5	5.8	1941	4	US-09-252-991A-6778	Sequence 6728, Ap
16	138.5	5.7	1200	4	US-09-252-991A-6282	Sequence 6282, Ap
17	137	5.6	756	4	US-09-252-991A-6106	Sequence 6106, Ap
18	137	5.6	4861	4	US-09-252-991A-7234	Sequence 7234, Ap
19	137	5.6	4403765	3	US-09-103-840A-2	Sequence 2, Appl
20	135.5	5.6	1413	3	US-09-328-352-2547	Sequence 2547, Appl
21	135	5.6	4411529	3	US-09-103-840A-1	Sequence 1, Appl
22	134	5.5	825	4	US-09-134-001C-2442	Sequence 2442, Ap
23	132	5.4	1974	4	US-09-252-991A-11111	Sequence 11111, A
24	129.5	5.3	1275	4	US-09-543-681A-590	Sequence 590, App
25	129.5	5.3	12127	4	US-08-961-527-148	Sequence 148, App
26	128.5	5.3	915	4	US-09-540-236-1467	Sequence 1467, Ap
27	128.5	5.3	1683	4	US-09-252-991A-11226	Sequence 11226, A
28	128.5	5.3	2085	4	US-09-252-991A-14016	Sequence 14016, A
29	128.5	5.3	2115	4	US-09-252-991A-14060	Sequence 14060, A
30	128.5	5.3	2397	4	US-09-252-991A-14210	Sequence 14210, A
31	128.5	5.3	3087	4	US-09-221-017B-81	Sequence 81, Appl
32	128	5.3	2217	4	US-09-252-991A-10720	Sequence 10720, A
33	128	5.3	2526	4	US-09-252-991A-10348	Sequence 10348, A
34	128	5.3	2921	4	US-09-252-991A-13447	Sequence 13447, A
35	127.5	5.2	951	4	US-09-252-991A-16386	Sequence 16386, A
36	127.5	5.2	1092	4	US-09-252-991A-16212	Sequence 16212, A
37	127.5	5.2	1530	4	US-09-252-991A-16005	Sequence 16005, A
38	127	5.2	10146	4	US-08-956-171E-243	Sequence 243, App
39	126.5	5.2	1305	4	US-09-328-352-944	Sequence 944, App
40	126.5	5.2	1503	4	US-09-252-991A-8482	Sequence 8482, App
41	126	5.2	1407	4	US-09-252-991A-11395	Sequence 11395, A
42	126	5.2	2205	4	US-09-252-991A-16465	Sequence 16465, A
43	126	5.2	2871	4	US-09-252-991A-16137	Sequence 16137, A
44	126	5.2	2256	4	US-09-252-991A-11431	Sequence 11431, A
45	126	5.2	38675	4	US-08-311-731A-135	Sequence 135, App

#### ALIGNMENTS

RESULT 1  
US-09-431-099-3  
Sequence 3, Application US/0941099  
Patent No. 6410705  
GENERAL INFORMATION:  
APPLICANT: Degussa-Höls AG  
TITLE OF INVENTION: Forschungszentrum Jülich GmbH  
TITLE OF INVENTION: New nucleotide sequences coding for the thr3 gene and process for  
FILE REFERENCE: 990079 BT  
CURRENT APPLICATION NUMBER: US/09/431,099  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 1909  
TYPE: DNA  
ORGANISM: Corynebacterium glutamicum ATCC13032  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (280)..(1746)  
OTHER INFORMATION: thr3-Gen  
US-09-431-099-3

#### Alignment Scores:

Pred. No.: 9,87e-264  
Score: 2432.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Gaps: 0

US-09-963-521-2 (1-489) x US-09-431-099-3 (1-1909)

QY 1 MetLeuSerPheAlaThrLeuArgGlyYArgIleSerThrValAspAlaAlaAlaAla 20  
|||||

Db 280 ATGTTGAGTTTTCGACCCCTTCGTGGCCGCAATTTCACAGTTGACCTCGCAAAAGCCCA 339  
 QY 21 ProProProSerProleuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal 40  
 Db 340 CTTCCGCCATCGCACTAGCCCCGATGTGATCTACAGCATTGTCAGAGGCGCGGTG 399  
 QY 41 MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp 60  
 Db 400 ATGAAATTGGCTCGAGAAATTGGCGAATTTTCTTCTTCAGATCGTCAAAATGAGTAC 459  
 QY 61 ThrIlyValGlnValArgAlaValThrSerAlaThrGlyLeuValTyrThrHisValAsp 80  
 Db 460 ACCAAGGTACAAAGTTCGAGAGTGAAGCTTCGCGTACGTTGTACTACACGCACTGGAT 519  
 QY 81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGlnArgLysMetProVal 100  
 Db 520 ATCAGCGTGAATACGATCACCATTCTTCACCAACATGGTGTGGAGAGAAAGATGCCGCT 579  
 QY 101 AsnValPheHisValValGlyLysLeuAspThrAsnPheseLysLeuSerGlyValAsp 120  
 Db 580 AACGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGAC 639  
 QY 121 ArgLeuIleArgSerIleGlnAlaGlyAlaThrProProGlnValAlaGlnLysIleLeu 140  
 Db 640 CGTTTGCCTTCATTCAGGCTGTGCGACCCCGCTTGAAGTTGCCGAGAAATCTCTG 699  
 QY 141 AspGlnLeuGlnGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyTyrAla 160  
 Db 700 GACGAGTTGAGACATCCCGCGCTCTTAGGTTTCCCTGTGGCTTGCTGGCTGGGCA 759  
 QY 161 MetMetGlyGlyAlaValAlaValLeuLeuGlyGlyTyrProlGlnValSerLeuIleAla 180  
 Db 760 ATGATGGTGTGCTGTGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 819  
 QY 181 PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyLysGlyLeuPro 200  
 Db 820 TTTATTCACGGGTTTCAGATATTGTCACACGATCATTTTGGGAAAGAGGTTTGCT 879  
 QY 201 ThrPhePheGlnAsnValAlaGlyGlyPheIleAlaThrLeuProAlaSerIleAlaTyr 220  
 Db 880 ACTTCTTCCAAAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAT 939  
 QY 221 SerLeuAlaLeuGlnPheGlyLeuGlnIleLysProSerGlnIleIleAlaSerGlyIle 240  
 Db 940 TCTTGTGGCGTTTCAGATATTGTCACACGATCATTTTGGGAAAGAGGTTTGCT 999  
 QY 241 ValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyAla 260  
 Db 1000 GTTGTGCTGTGGCAGGTTTACACTGCTGCAATCTCTGACGAGCGGCAACGCGCGCT 1059  
 QY 261 ProValThrAlaSerAlaArgPhePheGlnThrLeuLeuPheThrGlyIleValAla 280  
 Db 1060 CCGGTGACAGCAAGTGCAGATTTTTCGAAACACTCTGTTTACCGCGGCGCATTTGTTCT 1119  
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 QY 301 SerAlaAlaAlaProAsnTyrSerSerThrPheAlaArgIleIleAlaGlyIleValThr 320  
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 QY 321 AlaAlaAlaPheAlaValGlyCysTyrAlaGlnTyrPheSerValIleIleAlaGlyLeu 340  
 Db 1240 GCAGCGGCTTCGACGTGGTGTGTACGCGGAGTGTCTCGGTGATTAATGCGGCGCTT 1299  
 QY 341 ThrAlaLeuMetGlySerAlaPheTyrTyrLeuPheValAlaTyrLeuGlyProValSer 360  
 Db 1300 ACTGGCGTGAATGGGTTCTGCGTTTATTAACCTTCTGTTGTTATTTAGGCCCTCTCT 1359  
 QY 361 AlaAlaAlaIleAlaAlaThrAlaValGlyPheThrGlyGlyLeuLeuAlaArgArgPhe 380  
 Db 1360 GCCGCTGGATTTGCTGCAACAGCATGTGTTCACCTGCGTGTGCTTGCCTGCAATTC 1419

QY 381 LeuIleProProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400  
 Db 1420 TTGATTTCCACCGTTGATGTGTGGGATTTGCCGATACACCAATGCTTCAGGCTTAGCA 1479  
 QY 401 IleTyrArgGlyMetTyrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle 420  
 Db 1480 ATTTCACCGGAGATGATACGCCACCTCGAATGATCAACACTCATGGGTTTCCCAACATT 1539  
 QY 421 AlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValValLeuGlyGlnTyrPhe 440  
 Db 1540 GCGTGTCTTTAGCCACTGCTTCATCATCTGCGCTGCGCTGTGTGTGTGTGTGTGTGT 1599  
 QY 441 AlaArgArgLeuArgArgProProArgPheAsnProTyrArgAlaPheThrLysAlaAsn 460  
 Db 1600 GCCCGAGGCTAGCTGCTCCACACCGCTTACACCATCATCTGCTGATTTACCAAGCGAAT 1659  
 QY 461 GluPheSerPheGlnGlnGlnAlaGlnGlnAsnGlnArgGlnArgLysArgProLys 480  
 Db 1660 GAGTTCTCTTCCAGAGGAGAACTGAGCAGATCAAGCGCGCAGAGAAACGTCMAAG 1719  
 QY 481 ThrAsnGlnArgPheGlyAsnLysArg 489  
 Db 1720 ACTAATCAGAGATTCGTTAATAAAGG 1746

## RESULT 2

US-09-431-099-1

; Sequence 1, Application US/09431099

; Patent No. 6410705

; GENERAL INFORMATION:

; APPLICANT: Degussa-Höls AG

; TITLE OF INVENTION: New nucleotide sequences coding for the thrE gene and process for

; FILE REFERENCE: 990079 BT

; CURRENT APPLICATION NUMBER: US/09/431, 099

; CURRENT FILING DATE: 1999-11-01

; NUMBER OF SEQ. ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.1

; SEQ. ID NO. 1

; LENGTH: 2817

; TYPE: DNA

; ORGANISM: Corynebacterium glutamicum ATCC14752

; FEATURES:

; NAME/KEY: CDS

; LOCATION: (398)..(1964)

; OTHER INFORMATION: thrE-Gen

US-09-431-099-1

## Alignment Scores:

Pred. No.:	1,87e-263	Length:	2817
Score:	2432.00	Matches:	489
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-963-521-2 (1-489) x US-09-431-099-1 (1-2817)

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 Db 398 ATGTTGAGTTTTCGACCCCTTCGTGGCCGCAATTTCACAGTTGAGCTTCGCAAAAGCCCA 457  
 QY 21 ProProProSerProleuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal 40  
 Db 458 CTTCCGCCATCGCACTAGCCCCGATGTGATCTACAGCATTGTCAGAGGCGCGGTG 517  
 QY 41 MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp 60  
 Db 518 ATGAAATTGGCTCGAGAAATTGGCGAATTTTCTTCTTCAGATCGTCAAAATGAGTAC 577  
 QY 61 ThrIlyValGlnValArgAlaValThrSerAlaThrGlyLeuValTyrThrHisValAsp 80

Db 578 ACCAAGGTGCAAGTTCAGCGGTGACCTCTGCGTATGGCTCTGATACCATGTGAT 637  
QY 81 ILeThleuSbnThrlIethrIlePheThrsnlllegIyValGuaArgLysMetProVal 100  
Db 638 ATACAGTTGAATGCATCACCATTCTTCCAAACATCGGTGGAGAGAGATGCCGCTC 697  
QY 101 AsnValPheHisValValGlyLysLeuAspThrAsnPheserLysLeuSerGluValAsp 120  
Db 698 AACGTGTTTCAATGTTGGGCAAGTTGACACCAACTTCTCCAAACGTCTGAGGTGAC 757  
QY 121 ArgLeuIleArgSerIleGlnAlaGlyAlaThrProProGluValAlaGlyLysIleLeu 140  
Db 758 CGTTTGAATCGCTTCATTCAGCGCTGCTGCTACCCCGCTGAGGTTGCCGGAATAATCTG 817  
QY 141 AspGluLeuGluGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyTyrPala 160  
Db 818 GACGAGTTGAGCAATGCCTGCGCTTATGCTTCCCTGTTGCTTGGCTGGCGCA 877  
QY 161 MetMetGlyGlyAlaValAlaValLeuLeuGlyGlyGlyTyrPalaSerLeuIleAla 180  
Db 878 ATATGGGTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 937  
QY 181 PheIleThrsAlaPheThrIleIleAlaThrThrsPheLeuGlyLysLysGlyLeuPro 200  
Db 938 TTTATTACCGCGTTCAAGCATTCATCCACAGACGCTCATTTTGGGAAGAGGTTTGCT 997  
QY 201 ThrPhePheGlnAsnValValGlyGlyPheIleAlaThrLeuProAlaSerIleAlaTyr 220  
Db 998 ACTTCTTCCAAATGTTGTTGTTGTTTATGTCACAGCTGCTGCATGATGCTTNN 1057  
QY 221 SerLeuAlaLeuGlnPheGlyLeuGluIleLysProSerGlnIleIleAlaSerGlyIle 240  
Db 1058 TCTTTGGCGTTGAATTTGCTGTTGAGATCAACCAAGCCAGCATTCGATCTGGAAT 1117  
QY 241 ValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyAla 260  
Db 1118 GTTGTGCTGTGGCAGTTTGACATCTTGCAATCTCTGACAGACGGCATCACGGCGCT 1177  
QY 261 ProValThrAlaSerAlaArgPhePheGluThrLeuLeuPheThrGlyIleValAla 280  
Db 1178 CCGGTGACGCAAGTGCAGATTTTGAACACTCTGTTTACCGGCGCATGTTGCT 1237  
QY 281 GlyValGlyLeuGlyIleGlnLeuSerGluIleLeuHisValMetLeuProAlaMetGlu 300  
Db 1238 GCGGTGGTTTGGCGCATTCAGCTTCTGAATCTTGCAATGTCATGTTGCTGCCAAGAG 1297  
QY 301 SerAlaAlaAlaProAsnTyrSerSerThrPheAlaArgIleIleAlaGlyGlyValThr 320  
Db 1298 TCCGCTGACGACACTAATATTGCTGCTAATTGCGCCGCAATATCGCTGGTGGCTCAC 1357  
QY 321 AlaAlaAlaPheAlaValGlyCysTyrAlaGluTyrPheSerValIleIleAlaGlyLeu 340  
Db 1358 GAGGCGGCTTGGCAGTGGTGTGTTACGGGAGTGTCTCGGTATTAATTCGGGGCTT 1417  
QY 341 ThrAlaLeuMetGlySerAlaPheTyrTyrLeuPheValValTyrLeuGlyProAlaSer 360  
Db 1418 ACTGGCGTGAATGGTTCGCTTATTAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1477  
QY 361 AlaAlaAlaIleAlaAlaThrAlaValGlyPheThrGlyGlyLeuLeuAlaArgPhe 380  
Db 1478 GCCCGTGCAGATTGTCGCAACAGCAGTGTGTTCACTGGGTGCTTCCGCTGGATTC 1537  
QY 381 LeuIleProProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400  
Db 1538 TTGATTTCAACCGTTGATTTGCGCATTCGCGGCATCACCAATCTTCCAGGTCTACCA 1597  
QY 401 IleTyrArgGlyMetTyrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle 420  
Db 1598 ATTTACCGCGAATGTACGCCACTTGAATGATCAACATCATGAGGTTTCAACAACAT 1657  
QY 421 AlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValValLeuGlyGluTyrIle 440  
Db 1658 GCGGTGCTTAAAGCACTGCTTCACTTCGCGCTGGCGTGGTGGTGGTGGTGGTGGT 1717

QY 441 AlaArgPheLeuArgArgProProArgPheAsnProTyrArgAlaPheThrLysAlaAsn 460  
Db 1718 GCCCGAGAGGCTAGCTGCTCCACACGCTTCAACCCATCCGCTGATTTACCAAGCGAAT 1777  
QY 461 GluPheSerPheGlnGluGlnAlaGlyLysAsnGlnArgArgGluArgLysArgProLys 480  
Db 1778 GAGTTCCTCTTCCAGAGGAGAGCTGAGCAATTCAGCGCGCGGAGAGAAAACGTCCAAAG 1837  
QY 481 ThrAsnGlnArgPheGlyAsnLysArg 489  
Db 1838 ACTAATCAAGATTCGTTAATAAAG 1864

## RESULT 3

US-09-103-840A-2  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; TITLE OF INVENTION: TUBERCULOSIS  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09103,840A  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551  
; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
; OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

## Alignment Scores:

Pred. No.: 7 1e-51 Length: 4403765  
Score: 591.00 Matches: 167  
Percent Similarity: 50.86% Conservative: 69  
Best Local Similarity: 35.99% Mismatches: 174  
Query Match: 24.30% Indels: 54  
DB: 3 Gaps: 12

US-09-963-521-2 (1-489) x US-09-103-840A-2 (1-4403765)

QY 7 LeuArgGlyArgIleSerThrValAspAlaAlaLysAlaLysAlaProProSerProLeu 26  
Db 4179998 CTGCCGCGGCGC-----CGGATCCGCTGCCGCG 4180027  
QY 27 AlaProIleAspLeuThrAspHisSerGlnValAlaGly----- 39  
Db 4180028 GCG-----GCGCGCGGAGCGGACCTCGCGGAGATCGTGACCTGCACACC 4180075  
QY 40 -----ValMetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSer 57  
Db 4180076 CGGAAGGTGCTGACCTACCAATCCGCGCTCGCGGAGGATGTTGCTCGCGCTCGGC 4180135  
QY 58 AsnSerAspThrLysValGlnValArgAlaValThrSerAlaTyrGlyLeuTyrThr 77  
Db 4180136 ACCGCGGATGTCGTGCACAGCGGACGAGCGTCAAGGCTACAGCTCACCGATTC 4180195  
QY 78 HisValAspIleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGluArgLys 97  
Db 4180196 GTTGTGACATCACCGCTTACCAACATC---ATCGGTGCGCGGCTGCGGACCAAGACACT 4180252  
QY 98 MetProValAsnValPheHisValValGlyLysLeuAspThrAsnPheserLysLeuSer 117  
Db 4180253 CCGCGGTACACCAATCAGCGGCTCGGACCGCGGTCTCACTGACTACAGCGGCTGGCC 4180312

QY	118	GlulValAspArgLeuLeuLeuLeuSerIleGlnAlaGlyAlaThrProProGluValAlaGlu	137
Db	4180313	GAATCGATGACCTGCTTCCGCGAATACTCCGGGGCGGTGGCAATGACCAAGGCTCAC	4180372
QY	138	IleuIleuAspGluLeuGluGlnInserProAlaSerTyrGlyPheProValAlaLeuLeu	157
Db	4180373	GAGGCTATGACGAGGTTGACCGAAGCGGCCCACTTACCCGGCTGGCTGGGACCGGG	4180432
QY	158	GlyThrAlaMetMetGlyGlyAlaValAlaValLeuLeuGlyGlyGlyThrPpGlnValSer	177
Db	4180433	GGGGCGGGCGGCTTCGACTCGGCGGTCCCATGTGCTCGGGCGGAACCTGGCTGACTCG	4180492
QY	178	LeuIleAlaPheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyIleu	197
Db	4180493	GTCCTGGCTGCGCGGACGCTCTGGGTATGACCGAATGGAGCGGGCGGCTGAACCGGATC	4180552
QY	198	GlyLeuProThrPhePheGlnAsnValValGlyGlyPheIleAlaThrLeuProAlaSer	217
Db	4180553	GGGACCCCGTGTGTTCTTCCAGCCGGGTTCGGCGCGGGAGTCGGAGCCCTGGTCGGG	4180612
QY	218	IleAlaTyrSerLeuAlaLeuGlnPheGlyLeuGluIleLysProSerGlnIleIleAla	237
Db	4180613	CGCGCTTACCTGATCGCGGCGACG-----GATCGACCGGGCTGGTGGCC	4180657
QY	238	SerGlyIleValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIle	257
Db	4180658	ACCGGAATCGTTGTGCTGCTGCTGCGGATGACCTTGGTGGTTTGATGACGAGACCGGCTC	4180717
QY	258	ThrGlyAlaProValAlaThrAlaSerAlaAlaPhePheGluThrLeuLeuPheThrGly	277
Db	4180718	ACCGGAGTACATGCTCACCGCACTCGCCCGGCTTGGCCAGCCGCTTCTCGACCGCAGGG	4180777
QY	278	IleValAlaGlyVal-----GlyLeuGlyIleGlnLeuSer	289
Db	4180778	ATCGTCGTCGCGCATCTCATCTCGTTCGGGGCGGTCACCAATGCGGCATTCAGATGAA	4180837
QY	290	GluIleLeuHisValMetLeuProAlaMetGlnSerAlaAlaAlaProAsnTyrSerSer	309
Db	4180838	-----CTGCAATGTC-----GAGCAACACAGAGCTGGCCACCCCGGGCATGCCCTA	4180885
QY	310	ThrPheAlaArgIleIleAlaGly-----GlyValThrAlaAlaAlaPheAlaValGlyCys	328
Db	4180886	CGGATTCCTGTCGGCGTAAGCGGTGGCGGCTGTCGGCGGTGCTGACGATCGCAGAC	4180945
QY	329	TyrAlaGluTyrPseSerValIleIleAlaGlyLeuThrAla-----	342
Db	4180946	TATGGCGCGCTACGTTCTGTGGCCACCGCCGACACTCTGGCGGACTTCGCCAACTGGTG	4181005
QY	343	LeuMetGlySerAlaPheTyrTyrLeuPheValValTyrLeuGlyProValSerAlaAla	362
Db	4181006	CTCATCTGG-----CTCGCGCGCGCGGGGTTCGGCCGACGTGGTGCACCC	4181056
QY	363	AlaIleAlaAlaThrAlaValAlaGlyPheThrGlyGlyLeuLeuAlaArgArgPheLeuIle	382
Db	4181051	TGGACCGCGCGCATCGCGCGCTGCTTGGCCACCTGATCTCATCTGTCGGCGAGCTT	4181110
QY	383	ProProLeuIleIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAlaIleTyr	402
Db	4181111	CCCGCTGTGTAGCGCCACCGCCGCGCATACGCGATGCTGCCGGGCTTGGCGGTCTTC	4181170
QY	403	ArgGlyMetTyrAla-----ThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIleAla	421
Db	4181171	CGTGCGGTGTTCGCGCTGCGCTCATATGACACACCGAGCGGGTGTGACCCAGCTGTGTG	4181230
QY	422	ValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValAlaValLeuGlyGluThrIleAla	441
Db	4181231	GAGCGCGCGCCACATGCACTCGGCTTGGACCGGGGAGTGTGTGTGGGAGATGTTCTCGCC	4181290
QY	442	ArgArgLeuArg	445
Db	4181291	TCACTTTCGCG	4181302

```

US-09-103-840A-1
/ Sequence ID: Application US/09103840A
/ Patent No. 6294328
GENERAL INFORMATION
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 7,12e-51 Length: 4411529
Score: 591.00 Matches: 167
Percent Similarity: 50.86% Conservative: 69
Best Local Similarity: 35.99% Mismatches: 174
Query Match: 24.30% Indels: 54
DB: Gaps: 12

US-09-963-521-2 (1-489) x US-09-103-840A-1 (1-4411529)

QY 7 Leunrpglyatqgllsesthrvalasplalalaalyslalabpropopserproleu 26
Db 4187750 CTGGCGGCGGC-----CGCATCCGCTGCCCGTG 4187779
QY 27 Alaprolleaspleuthrasphisechlnavalaely-----39
Db 4187780 GCG-----GGCGGCGAGCGCGGACCTCGGAGATGATGACCTGCACACC 4187827
QY 40 -----Valmetamhleualaalarglleglyaspilleuleuseaserglythrser 57
Db 4187828 CGGAAGGTGCTGACCTGCATCCGCTCGGCTGCCGAGGATGTTGTCGTCCGCTCGC 4187887
QY 58 Asnserasprhlrylsvalgnvalargavalathriseralarylglyleuytyrtthr 77
Db 4187888 ACCGGGATGTCGTGCACCAAGCCAGAGCGTACTAGGCTCACAGCTACCGATTGC 4187947
QY 78 Hisvalaspllethrleuasnthrllethrlephethrasniileglyvalgluarlys 97
Db 4187948 GTTTCGACATCACCGTTACCAACATC---ATCGTTCGCGCTPAGCGACCAAGACACT 4188004
QY 98 Metprovalasnvalphehisvalvalaglylsleuasprthraampheaserlylseuer 117
Db 4188005 CGCGCGTTCACCATATATCGGTGCGTCCGACCGCGTCACTGACTACAGCGGCTGAC 4188064
QY 118 Gluvalaspargleullelarysertleinalaglyalatmrproprogluvalalaglu 137
Db 4188065 GAACTCGATCGACTCGTTCAGGCGGATACTCCCGGTGCGTGCAGTGCACAGCAAGCTCAC 4188124
QY 138 Lyslleuasgluleugluginserproalasertyrglypheprovalalaleu 157
Db 4188125 GAGGCTATGACGATTAAGCAAGCGCCACCCCTAACCGCGGTGCTGCAGACGCG 4188185
QY 158 Glytptpalametmetcglyvalavalavalaleuulgylglytytpginvalser 177
Db 4188185 GGCGCGCGGCGCTTGCACTCGCGCTCCGCAATGTTGCTCGCGGAACTCGCTGACTGC 4188244
QY 178 Leulleialaphellethrhalaphehthrillelealthrtnrserpheneglylyslrs 197
Db 4188245 GTCTTGCGTCCGTAACGTCTGCGTATCAACCACTGGCGGCTGCTGAACCGATTC 4188304
QY 198 Glyleuprothrphenephelinasnalvalaglyglypheallealthreuproblaser 217

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Db 4188305 GGGACCCCGTTCTTCTTACAGCGGCTGTCGGCGGGGATCGGACCCCTGCGCGT 4188364
QY 218 ILeaATyrSerLeuAlaLeuGlnPheGlyLeuGlnIleLysProSerGlnIleAla 237
Db 4188365 GCGGCTTACCTGATCGCGCGCAG-----GATCCGACCGCGCTGTGTGCC 4188409
QY 238 SerGlyIleValIleValLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIle 257
Db 4188410 ACCGGAATCGTTGGTGGCTCTCGGAGTACCTTGGTGGTTCGATGACGAGACGCGTCTC 4188469
QY 258 ThrGlyAlaProValThrAlaSerAlaArgPheGlnThrLeuLeuPheThrGlyIle 277
Db 4188470 ACCGGGTAACATCTACACCGACCTGCGCGGCTTGGCCACGCGCTTCTGACCGCAGG 4188529
QY 278 ILeValAlaGlyVal-----GlyLeuGlyIleGlnLeuSer 289
Db 4188530 ATCGTGTGCGGATCCATCTGTTGCGGGGCGTCAACCAATGCGCGCATTCGATCGAA 4188589
QY 290 GlnIleLeuHisValMetLeuProAlaMetGlnSerAlaAlaAlaProAsnTyrSerSer 309
Db 4188590 -----CTGATGTCTC-----GAGCGAACCAACGACCTCCACCCCGGCGATGCGCTA 4188637
QY 310 ThrPheAlaArgIleIleAlaGly-----GlyValThrAlaAlaAlaPheAlaValGlyCys 328
Db 4188638 CCGATTCTGCTCGCGGTACCGGTGCGGCGCTGTGCGGCTGTGCTGACGATGCGGAGC 4188697
QY 329 TyrAlaGlnTyrSerSerValIleIleAlaGlyLeuThrAla----- 342
Db 4188698 TATGCGCGCTACGTTGTGGCCACCGCGGAGCTCTCGCGCGGACCTCGCGCGAAGTGTGT 4188757
QY 343 LeuMetGlySerAlaPheTyrTyrLeuPheValValTyrLeuGlyProValSerAlaAla 362
Db 4188758 CTGATCGGA-----CTCGCGCGCGCGCGGTTCCGCGCAAGTGGTCCGACG 4188802
QY 363 AlaIleAlaAlaThrAlaValAlaGlyPheThrGlyGlyLeuLeuAlaArgArgPheLeuIle 382
Db 4188803 TGGACCGCGCGGATCGCGGCTGTGCGGCTTGTGGCCACCTGATCTCAATCGTGGCGAGCT 4188862
QY 383 ProProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAlaIleTyr 402
Db 4188863 CCGCGCTTGGTGCAGCGGCACCGCGGATCATGCGGATGTGCGGCGCTTGTGCGGTCTTC 4188922
QY 403 ArgGlyMetTyrAla---ThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIleAla 421
Db 4188923 CGTGGCGTGTTCGCTTCCGCGCAATGCACACCCGACGCGCGCTGACCCGACGTGCTG 4188982
QY 422 ValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValIleValLeuGlyGlnTyrPheIleAla 441
Db 4188983 GAAGCGCGCGGACCTGCACTCGCGCTTGGCAGCGGGGTGTGTGGTGGCGAGTTCCTGCGC 4189042
QY 442 ArgArgLeuArg 445
Db 4189043 TCACCATTCGCG 4189054

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/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
/ COMPUTER: HP Vectra 486/33
/ OPERATING SYSTEM: MSDOS version 6.2
/ SOFTWARE: ASCII Text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/956,171E
/ FILING DATE: 20-Oct-1997
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/009,861
/ FILING DATE: January 5, 1996
/ APPLICATION NUMBER: 08/781,986
/ FILING DATE: January 3, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mark J. Hyman
/ REGISTRATION NUMBER: 46,789
/ REFERENCE/DOCKET NUMBER: PB248P1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (240) 314-1224
/ TELEFAX: (301) 309-8439
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9834 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-08-956-171E-37
/
Alignment Scores:
Pred. No.: 4.7e-10 Length: 9834
Score: 190.00 Matches: 92
Percent Similarity: 38.26% Conservative: 66
Best Local Similarity: 22.28% Mismatches: 179
Query Match: 7.81% Indels: 77
DB: 4 Gaps: 12
US-09-963-521-2 (1-489) x US-08-956-171E-37 (1-9834)
QY 29 IleAspLeuThrAspHisSerGlnValAlaGlyValMetCAsnLeuAlaAlaArgIleGly 48
Db 8646 ATCACAATTATGATTAATAAACAAGATGTAATGTTCTTAATTGCAAGTAA----- 8593
QY 49 AspIleLeuLeuSerSerGlyThrSerAsnSerAspThrIysValGlnValAlaAlaVal 68
Db 8592 ---ATTTAATTGAATCAAGTGTCTGAAACATATCGAGTTGAAGATACAAATGAACCGTATC 8536
QY 69 ThrSerAlaTyrGlyLeuTyrTyrThrHis-----ValAspIle 81
Db 8535 GCACATAGTTATGATCTTATATATACATATAGTTTGTGATTCGAATTCGAATTAATTTT 8476
QY 82 ThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGlnArgIysMetProValAsn 101
Db 8475 TCATTAAACGATCGAACAAGTACAAGATTAATTCGTGTACAGAGCGT----- 8428
QY 102 ValPheHisValIleGlyIysLeuSphThrAsnPheSerIysLeuSerGlnValAspArg 121
Db 8427 -----ACAAACGATTTAAGAAAATCGCTTTAAAGAAATG 8392
QY 122 LeuIleArgSerIleGlnAlaGlyAlaThrProProGlnValAlaGlnIysIleLeuAsp 141
Db 8391 CTTTACGTAATAATTCAAATAAAGAACTCAACAAATTTGAAAGCTAAATCTGAATTAAT 8332
QY 142 GlnLeuGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyTyrAlaMet 161
Db 8331 CATTTAACGACATGATCAATACATATCTTTTAAAGAAATTTCTTTCAGTGGCAAT 8272
QY 162 MetGlyIleValAlaValLeuLeuGlyGlyIleGlyTyrPheGlnValSerIleLeuIleAlaPhe 181
Db 8271 GCATGTGCTTCTTCTTAATTATGTGTGTGTGTCGATCGATGATTTGATTCAGATC 8212

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RESULT 5  
 US-08-956-171E-37/C  
 Sequence 37, Application US/08956171E  
 Patent No. 6593114  
 GENERAL INFORMATION:  
 APPLICANT: Charles Kunsch  
 Gil H. Choi  
 Patrick S. Dillon  
 Craig A. Rosen  
 Steven C. Barash  
 Michael R. Fannon  
 TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
 NUMBER OF SEQUENCES: 5256  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: Maryland

```

QY 182 ILeThrAlaPheThrIleIleAlaThrSerPheLeuGlyLysGlyLeuProThr 201
DB 8211 ATTGGCGGGGATCCGACATTTTAACTTACGCTTGTGACGCTATATACAAATTAA 8152
QY 202 PhePheGlnAsnValValGlyGlyPheIleAlaThrLeuProAlaSerIleAlaTySer 221
DB 8151 TTTTCTCAGAG-----TTGTGCA-----GCCGCTGTGTCATATCC 8113
QY 222 LeuAlaLeuGlnPhe-----GlyLeuGlnIleLysProSerGlnIleIleAlaSer 238
DB 8112 ATTGCACCCACATTATTAATTAAGATTCGCAACCAATACAGATATCACTTACTATAGCC 8053
QY 239 GlyIleValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThr 258
DB 8052 AGTGCATATGACACTGTCCTCGTAATTAATTAACCAATCCATTCAGAGATTAATTAAGCG 7993
QY 259 GlyAlaProValThrAlaSerAlaArgPheGlnThrLeuLeuPheThrGlyIle 278
DB 7992 GGTGAATTACTTGCAGGTATGTCGCGGTGAGCTGCATTAAACAGATTCGCAATC 7933
QY 279 ValAlaGlyValGlyLeuGlyIleGlnLeuSerGlnIleLeuHisValMetLeuProAla 298
DB 7932 GGTGCTGTGTCGCAATC-----GTTTATTA----- 7906
QY 299 MetGlnSerAlaAlaAlaProAsnTySerSerThrPheAlaArgIleIleAlaGlyIle 318
DB 7905 -----ATCATTTAAGGAGG 7891
QY 319 ValThrAlaAlaAlaPheAlaVal-----GlyCySYrAlaGluTrp 332
DB 7890 ACTGTTAAAGCATGCTATTTTATTATTATTATTACATTCAGCTTATTAACACAGTAC 7831
QY 333 SerSerValIleIle-----AlaGlyLeuThrAla 342
DB 7830 TTTTCTCT-ATCATTTCATGACCAACCAAGCCTTATAGATGATGGATTTGTGGGT 7772
QY 343 LeuMetGlySerAlaPheTyTyLeuPheVal---ValTyLeuGlyProValSerAla 361
DB 7771 GCCATTGCATGACGATTTTACCAATTAACGATTAATTAAGATTGGAAGTTGGCGCT 7712
QY 362 AlaAlaIleAlaIleAlaThrAlaValGlyPheThrGlyGlyLeuLeuAlaArgArgPheLeu 381
DB 7711 TCATTTTGGAGCTTAATTTTAGGCTTAATGAGTCACTACTATGACGCGAGATATAA 7652
QY 382 IleProPheLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAlaIle 401
DB 7651 CGACCCGTAATTAATTAATGATAGTGCACGACATTAACATTAGTACCTGCTGTCAGCT 7592
QY 402 TyArgGly---MetTyAlaThrLeuAsnAspGlnThr 413
DB 7591 TATCAAGCAGCTGTTTATTAGTATCAAAATGATATATA 7553

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RESULT 6  
US-08-961-527-87/C  
Sequence 87, Application US/08961527  
Patent No. 6420135

GENERAL INFORMATION:  
APPLICANT: Charles Kunach  
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 391  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEO ID NO: 87
SEQUENCE CHARACTERISTICS:
LENGTH: 18436 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-87
Alignment Scores:
Pred. No.: 2.68e-07 Length: 18436
Score: 169.50 Matches: 106
Percent Similarity: 37.00% Conservative: 79
Best Local Similarity: 21.20% Mismatches: 195
Query Match: 6.97% Indels: 123
Gaps: 16
US-09-963-521-2 (1-489) x US-08-961-527-87 (1-18436)
QY 31 LeuThrAspHisSerGlnValAlaGlyValMetAsnLeuAlaAlaArgIleGlyAspIle 50
DB 7209 ATGGAAGAAATCAAAAGATTAATTAATCCGCTCATGTATGTATGTCAGGGGACATTT 7150
QY 51 LeuLeuSerGlyThrSer-----AsnSerAspThrLysValGlnValArgAla 67
DB 7149 CTCCTTAAAGTGCTCAGAAATCATCCATCGTGTAGAAAGATCCAGATTCGCAATC----- 7096
QY 68 ValThrSerAlaTyGlyLeuTyTyThrHisAlaSpIleThrIleAsnThrIleThr 87
DB 7095 -----GCGCAATTCGACAGGGATTTGGATTCGATGCTGCTGCCATGCCCTCCGCT 7045
QY 88 IlePhe-----ThrAsnIleGlyValGluArgLysMetProValAsnVal 102
DB 7044 ATCTTTTCTCTATGAAAAATACCAATATTTGGCGCAG-AGCGCGTGACCTCCTTCT 6986
QY 103 PheHisValValGlyLysLeuAspThrAsnPheSerLysLeuSerGluValAlaAspArgLeu 122
DB 6985 TAT-----AACATCGAAAAAGCTCGGAGGTGAACCAAGATT 6950
QY 123 IleArgSerIleGlnAlaGlyAlaThrProProGluValAlaGluLysIleLeuAspGlu 142
DB 6949 TCTGCTAGCTTAGTTGGGGGCGACATTGACTTAGAAACAGCCTTAAGCATTTGACGGCC 6890
QY 143 LeuGlnGlnSerProAlaSerTyGly-----TTPAlaMetMetGlyGlyValAla 151
DB 6889 TTGCAAGCCAAACCCCTCCCTATATCTAAAGTTGACAGTAACTGCTGCGACCTTTAGT 6830
QY 152 -----PheProValAlaLeuLeuGly-----TTPAlaMetMetGlyGlyValAla 166
DB 6829 GCTCCTTCTTTTTCAGTATGTTTAGCGGAATATCTACAGCAGCAGCTGGGCGAGAGTG 6770
QY 167 AlaValIleLeuGlyGlyGlyTyPheGlnValSerLeu-----IleAlaPhe 181
DB 6769 GCGACCTTATTTGTTTGGCTTTTCCCTCATGTGGAATAATTTATCGCATTTCCCTTT 6710
QY 182 IleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyLysGlyLeuProThr 201
DB 6709 GTGACAGCCTTT----- 6698
QY 202 PhePheGlnAsnValValGlyGlyPheIleAlaThrLeuProAlaSerIleAlaTySer 221

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Db      6697 -----GCTGAGACCTTGTCTTTGGGATA-----ATTGCCCAAGTT 6662
QY      222 LeuAlaLeuGlnPheGlnLeuGlnLeuProSerGlnLeuAlaSerGlyLeuAla 241
        |||||
Db      6661 TGGGCTGCGTACACAGGTTTTCCTCAACGCGACATTGATTATAGCTGGCGGTATG 6602
QY      242 ValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyLeuThrGlyAlaPro 261
        |||||
Db      6601 CCGTTTGTACAGGATATGCTTGAACCAATGCGGTCCGTATATTATGACCAACCATATA 6542
QY      262 ValThrAlaSerAlaArgPhePheGlnThrLeuLeuPheThrGlyLeuAlaGlyAlaGly 281
        |||||
Db      6541 AACCTGGATATGATAGATGTTGAATCCCTGCTCATTCCTCGCTTAAAGGGGACAGA 6482
QY      282 ValGlyLeuGlyLeuGlnLeuSerGlnLeuHisValMetLeuProAlaMetGlnSer 301
        |||||
Db      6481 ACTTCGTGCTGCTTGGT-ATTGATGAACTATATG-ACACTAACACACTTTTATTACAA 6424
QY      302 AlaAlaAlaProAsnThrSerSerThrPheAlaArgLeuAlaGlyValThrAla 321
        |||||
Db      6423 GCAGTAGCA-----AGTTTCTTGCCATATC----- 6397
QY      322 AlaAlaPheAlaValGlyCysTyrAlaGlnTrpSerSerValLeuLeuAlaGlyLeuThr 341
        |||||
Db      6396 ---ACTTTTAAATGCTACTCAATGTCACACGCTATGCTTACCTGAGGAGATTG 6340
QY      342 AlaLeuMetGlySerAlaPheTyrTyrLeuPheValValTyrLeuGlyProValSerAla 361
        |||||
Db      6339 GGCATAGCTGCTGGCAATCTATCTCTCTCTCAAGAACCGCAACATGCTATGCT 6280
QY      362 AlaAlaIleAlaAlaThrAlaValGlyPheThrGlyLeuLeuAlaArgArgPheLeu 381
        |||||
Db      6279 ACCTTCATGACACCTTATGCTTCTGTCAGCAGATTTAAGTATCTTTATAG 6220
QY      382 IleProProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAlaIle 401
        |||||
Db      6219 AACCTGCTGCTGCTTATCTTGGCCATTTTGGCACCGCTGCTCAGGTATCTCTCC 6160
QY      402 TyrArg-----GlyMetTyrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsn 419
        |||||
Db      6159 TACCGAACAACTGCTTTTGTGACA-----GGGACATATAT 6121
QY      420 IleAlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValValLeuGlyGlnTr 439
        |||||
Db      6120 AAAGCACTGGCAAGTCGACCTTGTTCATGTTGGTGGTATCTCTATTTGGAATG 6061
QY      439 PileAla----- 443
        |||||
Db      6060 GCTAGCGGACAGTATCTCAGACTCTATCATTTATATATAAAACACATGAGATGTAG 6001
QY      443 GLeuArgArgProProArgPhe----- 450
        |||||
Db      6000 ACTTTACAGAAATAAAGAAATTTTCGAAAAATGAGATAAATTAATGATAACGCTTCT 5941
QY      451 -----AsnProTyrArgAlaPheThrLys--AlaAsnGlnPheSerPheGlnGlu 466
        |||||
Db      5940 ATATGTGCGAAGATCCGCACTTATGAAAGAAATTTGGCTGATTTGATCCACGAA 5883

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; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 23210
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 28
; OTHER INFORMATION: a or g or c or t, unknown, or other
; PUBLICATION INFORMATION: Incyte template ID No. 6632636 17
; US-09-596-002-17

Alignment Scores:
Pred. No.: 1.26e-06 Length: 23210
Score: 165.00 Matches: 95
Percent Similarity: 37.84% Conservative: 84
Best Local Similarity: 20.08% Mismatches: 207
Query Match: 6.78% Indels: 88
DB: 4 Gaps: 14

US-09-963-521-2 (1-489) x US-09-596-002-17 (1-23210)

QY      13 ThrValAspAlaIleAlaValAlaProProSerProLeuAlaProIleAspLeuThr 32
        |||||
Db      22074 ACATTCACAGCCACCAAAAGTCACCA-----ATGACTAATTTGACC 22033
QY      33 Asp-----HisSerGlnVal 37
        |||||
Db      22032 GACGAGATGCCACGATTTTATTGATACGCATACACGCCGCTTAACATGCTACGCA 21973
QY      38 AlaGlyValMetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerGlyThrSer 57
        |||||
Db      21972 CAACGATACCTGCTTATGATACCGCTGCTTACTACTCATGCAATATGCTGACAG 21913
QY      58 AsnSerAspThrLysValGlnValAlaGlnAlaValThrSerAlaTyrGlyLeuTyrTyrThr 77
        |||||
Db      21912 TCTGTCGTGCTGCTTATTAACAAAGCGCTTGGGCGGCACTTGAGATGAGTGT 21853
QY      78 HisValAspIleThrLeuAsnThrIleThrIlePheThr----- 90
        |||||
Db      21852 GAGTCGGTTCGACATTTATATGCGGTACCTTAACCACTTATATACAGGCTGCTATC 21793
QY      91 -----AsnIleGlyValGlnArgLysMetProValAsnValPhe 103
        |||||
Db      21792 ACAACGTCGAGAAATACCGTTCATCAAGGCATTAATGTCAGATCTTAGTACAAATTTCA 21733
QY      104 HisValValGlyLysLeuAspThrAsnPheSerLysLeuSerGlnVal----- 119
        |||||
Db      21732 CAATTTATCTTAAGCGCGCAAAATCATCAAGCAATCAATCTATTTGTTAAACCCCA 21673
QY      120 -----AspArgLeuIleArgSerIleGlnAlaGlyAlaThrProProGlnValAlaGln 137
        |||||
Db      21672 AGCCATGACGCATGATATCAGTAGCGTAAACAAGG----- 21637
QY      138 LysIleLeuAspGlnLeuGlnLeuSerPro-----AlaSerTyrGlyPhe 152
        |||||
Db      21636 -----TTTGATGCCATCTACCAAACTGCTATCTATCAATCTTGGTATCTTTTGTG 21583
QY      153 ProValAlaLeuLeuGlyTyrPalaMetMetGlyGlyAlaValAlaValLeuLeuGlyGly 172
        |||||
Db      21582 GCGCTATCATGCGCAGTTTCCATTTTAAACGTCACACTTGTG----- 21535
QY      173 GlyTyrGlnValSerLeuIleAlaPheIleThrAlaPheThrIleIleAlaThrThrSer 192
        |||||
Db      21534 -----ATTGCTCTGATTACTTTATTTGCGAGTTTGTGGCATGGATGGATGGGTAG 21484
QY      193 PheLeuGlyLysLysGlyLeuProThrPhePheGlnAsnValValGlyGlyPheIleAla 212
        |||||
Db      21483 TATCTTTAAAGCAACATTTTATATCTTTTGTGCTGCTATGATACGCAATTTACCGCA 21424

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RESULT 7
US-09-596-002-17/c
; Sequence 17, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NOCLECTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-008-4 US
; CURRENT APPLICATION NUMBER: US/09/596,002
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18

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; Sequence 6445, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6445
; LENGTH: 915
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-6445
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Alignment Scores:
Pred. No.: 7,62e-07 Length: 915
Score: 146.50 Matches: 76
Percent Similarity: 32.69% Conservative: 25
Best Local Similarity: 24.60% Mismatches: 136
Query Match: 6.02% Indels: 72
DB: Gaps: 8
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US-09-963-521-2 (1-489) x US-09-252-991A-6445 (1-915)

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QY 151 GtPhPheProValAlaLeuLeuGlyTTPAlaMetMetGlyGlyAlaValAlaValLeuLeu 170
Db 754 GGGCTTGCAGACAGCGCTTAGAGGGCTGTCGGGCGCGCGCTTGTCTGCC---CGC 698
QY 171 Gly-GlyGlyTTPGlnValSerLeuIleAlaPheIleThrAlaPheThrIleIleAla 190
Db 697 GGCAGGCGCTTGCAGAGCGCGCTGAGGCGCGCTGCCGCGGCGCTGGAGTCCCGCAGG 638
QY 190 rThrSerPheLeuGlyLysLysGlyLeuProThrPhePheGlnAsnValAlaGlyLys 210
Db 637 CTTGCGACGACGAGCGGCTGGCGGCTG-----GTTGCGGACAGGTTT 596
QY 210 eIleAlaThr---LeuProAlaSerIleAlaTyrrSerLeuAlaLeuGlnPheGlyLeu 229
Db 595 CGGCGCTACGGGCTTTCGCCGAGCTTGGCGCGCTTTCGCCGACGCTTC----- 544
QY 229 uIleLysProSerGlnIleIleAlaSerGlyIleValAlaValLeuLeuAlaGlyLeuThr 249
Db 543 -----GCAAGCGCTTGGCTGCGACGCTTGGCGCGCGCGGCGGATTT 506
QY 249 uValGlnSerLeuGlnAspGlyIleThrGlyAlaProValThrAlaSerAlaArgPhe 269
Db 505 CGCGACAGGCTTGGCGCGGCTTTCGCCGAGGCTTTCGACGCTTGGCTTGGCGGCTT 446
QY 269 eGlnThrLeuLeuPheThrGlyGlyIleValAlaGlyValAlaGlyLeuGlyIleGlnLeu 289
Db 445 CGCGGCTGCGGCTTTCGCCGCGGCTTTCGCCGCTTTCGCCGACGCTTTCGCCCGG 386
QY 289 rGlnIleLeuHisValMetLeuProAlaMetGlnSerAlaAlaAlaProAsnTyrSer 309
Db 385 CTTGGCGGCGGCTTTCGCCGCTTTCGCCGAGGCTTTCGCCGCGGCTTTCGCCGAC 326
QY 309 rThrPheAlaArgIleIleAlaGlyGlyValThrAlaAlaAlaPheAlaValAlaGly 329
Db 335 AGGCTTTCGCGCGGCTTTCGCCGCGGCTTTCGCCGCTTTCGCCGCGGCTTTCGCC 266
QY 329 rAlaGlnTTPSerSerValIleIleAlaGlyLeuThrAlaLeuMetGlySerAlaPhe 349
Db 265 CGCGGCTTTCGACAGGCTTTCGCCGCTTTCGCCGCTTTCGCCGCTTTCGCCGCGG 206
QY 349 rTyrLeuPheValValTyrLeuGlyProValSerAlaAlaAlaAlaAlaThrAla 369
Db 205 C-----GCCGAGGCTTTCGCCGCGGCTTTCGCCGCTTTCGCCGAC 176
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QY 369 lGlyPheThrGlyLysLeuLeuAlaArgPheLeuIleProProLeuIleValAla 389
Db 175 AGGCTTTCGACAGCGGCTTTCGCCG----- 151
QY 389 eAlaGlyIleThrProMetLeuProGlyLeuAlaIleTyrArgGlyMetTyrAlaThr 409
Db 151 ----- 151
QY 409 uAsnAspGlnThrLeuMetGlyPheThrAsnIleAlaValAlaLeuAlaThrAlaSer 429
Db 150 -----GCTTTCGCCGCTTTCGCCGCTTTCGCCGAGGCTTTCGCCGCGC 110
QY 429 rLeuAlaAlaGlyValValLeuGlyLysTTPAlaAlaArgPheLeuArgPhePro 449
Db 109 CTTGCGACGAGGCTTTCGCCGCTTTCGCCGCTTTCGCCGCTTTCGCCGAGGCTTTC 61
QY 449 gPheAsnProTyrArgAlaPheThr 457
Db 60 -----TTGCCAGAGGCTTTCCTTAC 40
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RESULT 10

US-09-252-991A-6023  
; Sequence 6023, Application US/09252991A  
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 6023

; LENGTH: 1806

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

; US-09-252-991A-6023

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Alignment Scores:
Pred. No.: 2,32e-06 Length: 1806
Score: 146.50 Matches: 76
Percent Similarity: 32.69% Conservative: 25
Best Local Similarity: 24.60% Mismatches: 136
Query Match: 6.02% Indels: 72
DB: Gaps: 8
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US-09-963-521-2 (1-489) x US-09-252-991A-6023 (1-1806)

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QY 151 GtPhPheProValAlaLeuLeuGlyTTPAlaMetMetGlyGlyAlaValAlaValLeuLeu 170
Db 517 GGGCTTGCAGACAGCGCTTTCGCCGAGGCTTTCGCCGCTTTCGCCGAGGCTTTCGCC 573
QY 171 Gly-GlyGlyTTPGlnValSerLeuIleAlaPheIleThrAlaPheThrIleIleAla 190
Db 574 GGCAGGCGCTTTCGCCGAGGCTTTCGCCGAGGCTTTCGCCGAGGCTTTCGCCGAG 633
QY 190 rThrSerPheLeuGlyLysLysGlyLeuProThrPhePheGlnAsnValAlaGlyLys 210
Db 634 CTTGCGACGACGAGGCTTTCGCCGCTTTCGCCGCTTTCGCCGCTTTCGCCGAGGCTT 675
QY 210 eIleAlaThr---LeuProAlaSerIleAlaTyrrSerLeuAlaLeuGlnPheGlyLeu 229
Db 676 CGCGGCTTTCGACAGGCTTTCGCCGCTTTCGCCGCTTTCGCCGCTTTCGCCGAGGCTT 727
QY 229 uIleLysProSerGlnIleIleAlaSerGlyIleValAlaValLeuLeuAlaGlyLeuThr 249
Db 728 -----GACGCGGCTTTCGCCGCTTTCGCCGCTTTCGCCGAGGCTTTCGCCGAG 765
```

QY 249 uValGlnSerLeuGlnAspGlyLeuThrGlyAlaProValThrAlaSerAlaArgPhe 269  
Db 766 CGCCACAGAGCTTGGCCGCGCTTCCGCCGACAGCTTCGACAGTGGCTTGGCTCCGCGCTT 825  
QY 269 eGluThrLeuLeuPheThrGlyGlyLeuValAlaGlyValGlyLeuGlyLeuGln 289  
Db 826 CGCGGCTGCGGCTTGGCCGCGCTTGGCCGCTTGGCCGCTTGGCCGCTTGGCCGCTT 885  
QY 289 rGluLeuLeuValMetLeuProAlaMetGlnSerAlaAlaProAlaSerAla 309  
Db 886 CTGGCGCGCGGCTTGGCCGCTTGGCCGCTTGGCCGCTTGGCCGCTTGGCCGCTT 945  
QY 309 rThrPheAlaArgGlyLeuAlaGlyValThrAlaAlaPheAlaValGlyGly 329  
Db 946 AGCGCTTGGCGCGCTTGGCCGCTTGGCCGCTTGGCCGCTTGGCCGCTTGGCCGCTT 1005  
QY 329 rAlaGluTrpSerSerValLeuLeuAlaGlyLeuThrAlaMetGlySerAlaPhe 349  
Db 1006 CGCGGCTTGGCGCGCTTGGCCGCTTGGCCGCTTGGCCGCTTGGCCGCTTGGCCGCTT 1065  
QY 349 rTyrLeuPheValValTyrLeuGlyProValSerAlaAlaAlaAlaAlaAla 369  
Db 1066 C-----GCCGACAGCTTGGCCGCTTGGCCGCTTGGCCGCTTGGCCGCTT 1095  
QY 369 lGlyPheThrGlyGlyLeuLeuAlaArgArgPheLeuLeuProLeuLeuValAla 389  
Db 1096 AGCGCTTGGCGCGCTTGGCCGCTTGGCCGCTTGGCCGCTTGGCCGCTTGGCCGCTT 1120  
QY 389 eAlaGlyLeuThrProMetLeuProGlyLeuAlaAlaTyrArgGlyMetTyrAlaThr 409  
Db 1120 ----- 1120  
QY 409 uAsnAspGlnThrLeuMetGlyPheThrAsnAlaValAlaLeuAlaThrAlaSer 429  
Db 1121 -----GGCTTGGCCGCGCTTGGCCGCTTGGCCGCTTGGCCGCTTGGCCGCTT 1161  
QY 429 rLeuAlaAlaGlyValValLeuGlyGlyTrpAlaAlaArgArgLeuArgArgPro 449  
Db 1162 CTTCGACAGAGCTTGGCCGCTTGGCCGCTTGGCCGCTTGGCCGCTTGGCCGCTT 1210  
QY 449 gPheAsnProTyrArgAlaPheThr 457  
Db 1211 -----TTGCCACAGCTTCTTCAC 1231

RESULT 11  
US-09-107-532A-248  
Sequence 248: Application US/09107532A  
Patent No. 6583375  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESS: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:  
NAME: Atinello, Pamela Deneka  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781) 893-5007  
TELEFAX: (781) 893-8277  
INFORMATION FOR SEQ ID NO: 248:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1896 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...1896  
SEQUENCE DESCRIPTION: SEQ ID NO: 248:  
US-09-107-532A-248

Alignment Scores:  
Pred. No.: 5,47e-06 Length: 1896  
Score: 143.50 Matches: 98  
Percent Similarity: 37.73% Conservative: 68  
Best Local Similarity: 22.27% Mismatches: 162  
Query Match: 5.90% Indels: 113  
Gaps: 21

US-09-963-521-2 (1-489) x US-09-107-532A-248 (1-1896)

QY 88 lPheThrAsnIleGlyValGluArgLysMetProValAsnValPheHisValValGly 107  
Db 107 ATATTGTCGATTTGTCGAGCGAAGAAATGTCACG-AAATGTTTACCATTTGCGACA 165  
QY 108 LysLeu-----AspThrAsnPheSerLysLeuSerGluVal 119  
Db 166 AGGTTAGCGCTTACCTTAAGAAATATAGAACGACATATAGAGAAAGCTAGACACTA 225  
QY 120 AspArgLeuIleArgSerIleGlnAlaGlyAlaThrProGluValAlaGluLysIle 139  
Db 226 GAAGTGTGATCATCTAGTCGAAGCTGACGAAGATGTTCAAGTCGTAAGTGAAGAAATGCA 285  
QY 140 LeuAspGlu-----LeuGluGlnSerProAlaSer 149  
Db 286 GTAATGAAAGTATGACGATTTATCCAAACAAATGAAACTAGAGATGATGATCTAGT 345  
QY 150 -----TyrGlyPheProValAlaLeuGlyTyr-----Ala 160  
Db 346 GGAAGAGAGCACTGAGAAAAAGGCACTTTTAACTCTTTATATGACATGATGCCCGCT 405  
QY 161 MetMetGlyGlyAlaValAlaValLeuLeuGlyGlyTyrGlnValSerLeuIleAla 180  
Db 406 GTTTTGGCCCGACCTTAGCGCTCTTGGCAGAAAGTGTGATCAAGAGTACTCGCC 465  
QY 181 PheIleThrAlaPheThrIleIleAlaPheThrSerPheLeuGlyLysGlyLeuPro 200  
Db 466 TTATGTACAGAGTTGAAATTTATTACTACTGAAAT-----GGAACCTAT 510  
QY 201 ThrPhePheGlnAsnValValGlyGlyPheIleAlaThrLeuProAlaSerIleAlaTyr 220  
Db 511 ATCATTTGATGACGACGACGATGATGATTTTCTATTTCTGCTATATTTTGGCAATAT 570  
QY 221 SerLeuAlaLeuGlnPheGlyLeuGluIleLysProSerGlnIleIleAlaSerGlyIle 240  
Db 571 ACTGCTGCAAAAAAGTCAATACAGAT-----CGTTTCATGCTATGTTAT 618  
QY 241 ValValLeuLeuAlaGlyLeuThrIleuValGlnSerLeuGlnAspGlyLeuThr----- 258  
Db 619 GCAGACGCTTCTGTTATCTTACGATTTGTCAGTGCATATATGATATGATTAACCTTGCGCA 678



; PRIOR APPLICATION NUMBER: US 60/094,100  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 7755  
 ; LENGTH: 1581  
 ; TYPE: DNA  
 ; ORGANISM: *Pseudomonas aeruginosa*  
 US-09-252-991A-7755

Alignment Scores:	
Pred. No.:	5.27e-06
Score:	142.50
Percent Similarity:	35.00%
Best Local Similarity:	22.68%
Query Match:	5.86%
DB:	4
Length:	1581
Matches:	127
Conservative:	69
Mismatches:	175
Indels:	190
Gaps:	26

US-09-963-521-2 (1-489) X US-09-252-991A-7755 (1-1581)

QY	21	ProProPro-----	-----SerProLeuAlaProLeu-AspLeu	32
Db	33	CCACCGCCATGCCACTGCATGCAGCAATATCATAGGCTCTTCCACCCCGTCGCAC		92
QY	32	AspHisSerGlnValAlaGlyValMetAsnLeuAlaAlaArgileGlyAspIleLeu		52
Db	93	GCGACATCTGCG-----	-----CTGGCTGAAGGACCGGGAAGTACTTG	134
QY	52	userSerGlyThrSerAsnSerAspThrLysValGlnValArgAlaValThrSerAla		72
Db	135	TCGAGCAGACCAACCCGTTCCAGATCCGGGCTCGGC-----	-----CGCAAGTTCCAGACGACGTA	191
QY	72	r-GlyLeuYrYrThrHisValAspIleThrLeuAsnThrIleThrIlePheThrAsnI		92
Db	192	CCGGCTCTCCACGATCCACCGTATCGGTACCTCGCCACCTTG-----		235
QY	92	IeGlyValGluArgLysMetProValAsnValPheHisValValGlyLysLeuAspThrA		112
Db	236	-----CAACGCGCCGGTCTCGGTGACCAACGCGCGGGTCGACG-----	-----TGCA	278
QY	112	snPheSerLysLeuSerGlnValAspArgLeuIleArgSerIleGlnAla-----		128
Db	279	ACTTCTTCAAGCGCAACGAG-----	-----GAGACATCCAGGCGCTTCCCTGCACC	323
QY	129	-----	-----GlyAlaThrProProGluValAlaGluLysI	139
Db	324	AACTCGCGCAGACGCTGTAAAGCAGACGCTCGCTCCACCCCA-----		367
QY	139	IeLeuAspGluLeuGlnGlnSerProAlaSerYrGlyPheProValAlaLeuLeuGlyT		159
Db	368	-----CCTCCAGTCCGAGAGCTGCAGCCGATCCGGCGGTCTTCTGTCTC		413
QY	159	xPalaMetMetGlyGlyAlaValAla-----	-----ValLeuLeuGly-----	171
Db	414	TGCTTTATTCGCGCTTTCATCGATGTAACACGCAATTCGTATCATCAAGGGCGTGTGCCG		473
QY	172	-----	-----GlyGlyTPGAlnValSerLeuIleA	180
Db	474	AGGTGCGCGGCGACCTGCGGGTATCATTTCCACGCGCGGCTGAGTCGATGAGCGGCTACG		533
QY	180	IaPheIleThrAlaPhe-----	-----ThrIleIleAlaThrThrSerPheLeuGlyL	196
Db	534	CCTTGCCCGTGGCTTCGGCGCCCGCTGATGGCATGGCCACCGCGCCGCTGGAGCGCA		593
QY	196	YelYagIleuProThrPhePheGlnAsnValAlaGlyIlePheIleAlaThrLeuProA		216
Db	594	AGAAACCTGCTCGCG-----	-----CTGATGGCATCTTCATGTC-----	632
QY	216	IaSerIleAlaYrSerSerLeuAlaLeuGlnPheGlyLeuGluIleLysProSerGlnIleI		236
Db	633	GCAACTGCTCTGCGGGTGGCGCAACATACGAGCTG-----		670
QY	236	IeAlaSerGlyIleValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAsp		256

Db 671 -----CTGATGCTGGG-----CGATTCGACACCGCTCGCATG 707  
 QY 256 IYIETHRGYALAPROVALTHRALASERIALARGPHEGIIUTHRLEUENUPHEHNG 276  
 Db 708 GC-----GCCCTTCCTCGGC-----ATCG 725  
 QY 276 IYGIYILEVALAGLYVALGYLEUGLYILEGIMUSEERGIULEUHIIVALMETL 296  
 Db 726 GCTGGTGATGCGCGCC----- 742  
 QY 296 EUPROALAMETGUSEERALAALAPROASNTRYSERERTHRPHEALARGILELEA 316  
 Db 743 -----AGCTCGTGCGCGCCAGACCGACTTCGCGCGTAGCGCTGATGT 788  
 QY 316 IAGLYGVVALTHRALAAL-----ALAPHEALVALGILCYST 329  
 Db 789 TCACCGGCTGACCCCTGCGCAACGTGCTGCGCGCTGCGGTGATCCGCGTCCGACAG 848  
 QY 329 YRHALGLUTPSEER-----VALLEILEAGLYLEUTHRALAUMETG 345  
 Db 849 AAGCGGCGTGGCGCGACCTTCTGGTGTGACCTGATCGCGTGTGCTTCGCG 908  
 QY 345 IYSERALA-----PHEITYRILEUP 352  
 Db 909 GCCTGCGCGGCTGCTGCGCAACGACCGAGAGAGAAGATGTGACCTGCGCACAGAAA 968  
 QY 352 HEVALVALYRLEUGLYPROVALSERIALAALALEALALEALATHRALVALGYPET 372  
 Db 969 TGTCCGCGCTGAAGAACCGCTGCTGCTGCTGCTGCGCGGACACCGCTGTGCTG 1025  
 QY 372 HNGLYLYLEUENUALARGARGPHEULEUPROPROLEUILEVALALEALAGLYI 392  
 Db 1026 CCGCTCGATGTTGCGCTGTTTCACTACCTGCGCGCGCTGCTGCGGAAGTACCGGG 1085  
 QY 392 IETHPRO-----METLEUPROGLYLEUALA----- 400  
 Db 1086 TTAGCCCGCGCGCGCGTGCACCTGACCTGTGCTGATCGGCGTGCACCGTGGCA 1145  
 QY 401 --ILETRYARGIYMETYRYALATHRLEUASNPGLINTHRLEUMETGLYETHIRASNI 420  
 Db 1146 AGGTGATCGGCGCGCGCTCGCGACTGCGCTGGGACACCAATGGCGCGGTTCG 1205  
 QY 420 LEALVALALALEUALATHRALA-----SERSERLEUALAALAG 433  
 Db 1206 CGCCATGCGGCGTGTCTCGCGCTGTTACGTGACGTGACAGCAGGCGCTGCTCGCG 1265  
 QY 433 IYVALILEUGLYGLUTRPILEALARGARGLEUARGARGPROARHPHEANPROT 453  
 Db 1266 AATATCACCTGTTCTTCTGTGGGC--CGCGCGCGCTTCGCGCGGTGACGATC 1324  
 QY 453 YRARGALAPHEHTRYALALA-----ANGIUP 462  
 Db 1325 AACGTGTCGCGCTGCGCGCATGCGCGCGCAACCTGTGCGGACCTGTGAATCGGCGCC 1384  
 QY 462 HESERHEGIIUGLIUGLIALAGLIUNASNGIARGARGIARGIYSAARGPROLYS 480  
 Db 1385 TTCACGTGCGCAACGCGCTCGCGCGCTGCGGCGGCGCAAGCTATGACACAG 1440  
 RESULT 14  
 US-09-252-991A-6891  
 ; Sequence 6891, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27



```

; LENGTH: 1941
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6728

Alignment Scores:
  Pred. No.:      1,24e-05      Length:      1941
  Score:          140.50        Matches:      107
  Percent Similarity: 34.87%    Conservative: 82
  Best Local Similarity: 19.74% Mismatches:    189
  Query Match:      5.78%      Indels:       165
  Db:               4          Gaps:         23

US-09-963-521-2 (1-489) x US-09-252-991A-6728 (1-1941)

QY 10 ArgIleSerThrValAspAlaAlaAlaPro----- 21
Db 1851 CGGCGCGGACGCTTCTCGTGGTGGCGTCCGACGACGCGCAACGGCGTCTGG 1792
QY 22 -----ProProSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGly 39
Db 1791 ATGACACCGCGCTTCG-----ACTACCATTCGCGCGCGCGCGCGCGAC 1750
QY 40 ValMetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSer 59
Db 1749 GCTCCCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1690
QY 60 AspThrIleValAlaAlaArgAlaValThrSerAlaTyrglyLeuTyrglyThrHisVal 79
Db 1689 CAGCAACCGGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1630
QY 80 AspIleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValAlaGlyValMetPro 99
Db 1629 GGGCTGACCTTCTTTCGCGCGACGATGACCGCGC----- 1594
QY 100 ValAsnValPheHisValValGlyLeuAspThrAsnPheSerIleuSerGluVal 119
Db 1593 -----GGCACCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1570
QY 120 AspArgLeuIleArgSerIleGlnAlaGlyAlaThrProGluValAlaGlyValIle 139
Db 1570 ----- 1570
QY 140 LeuAspGluLeuGluGlnSerProAlaSerTyrglyPheProValAlaLeuLeuGlyTyr 159
Db 1569 TACGACGACCTTC-----TTCTCGCGCGCGCGCGCGCGCGCGCGCGCG 1534
QY 160 AlaMetMetGlyValAlaValAlaValLeuLeuGlyGlyTyrPdpGlnValSerIle 179
Db 1533 CTGATGCTGGCGCTGTACACGCGCATCTCGGCTTCATCGCGCGCGCGCGCGCGCG 1474
QY 180 AlaPheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyValGlyGlyLeu 199
Db 1473 ACCGACCTGCGGCGCATTTACTCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1414
QY 200 ProThrPhePheGlnAsnValValGlyGlyPheIleAlaThrLeuProAlaSerIle--- 218
Db 1413 GCT-----CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1363
QY 219 ---AlaTySerLeuAlaLeuGlnPheGlyLeuGluIleuysProSerGlnIleIleAla 237
Db 1362 CCCAAATATCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1303
QY 238 SerGlyIleValValLeu-----LeuAlaGlyLeuThrLeuValAlaGlnSer 252
Db 1302 GGAAGCGGTGATGACCTTCACGCGTGTCTTCGCGCATCGCGCGCGCGCGCGCGCG 1243
QY 253 LeuGlnAspGlyIleThrGlyAlaProValThrAlaSerAlaArgPhePheGluThrLeu 272
Db 1242 ATC-----GGGCTCCCGCGCGATGCTGTTCTCGGACACTACTCGGATGCGCGGTG 1189
QY 273 LeuPheThrGlyGlyIleValAlaGlyValAlaGlyLeuGlyIleGlnLeuSerGluIleLeu 292

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```

Db 1188 CGGACGCGCGCGCGCGCTGCGCGCG-----CTGACGACGATG----- 1153
QY 293 HisValMetLeuProAlaMetGluSerAlaAlaAlaProAsnTygSerThrPheAla 312
Db 1152 -----ACGCGAGCGCGCGCGCGCTGAGCTTCGACCGCGGATC 1117
QY 313 ArgIleIleAlaGlyGlyValThrAlaAlaAlaPheAlaValAlaGlyCysTygAlaGluTyr 332
Db 1116 GCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1057
QY 333 -----SerSerValIleIleAlaGlyLeuThrAlaLeuMetGlySerAla 347
Db 1056 GCGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 997
QY 348 PheTygTygLeuPheValValTygLeuGlyProValSerAlaAlaIleAlaAlaThr 367
Db 996 CTGATGTATCATCTTC-----GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 949
QY 368 AlaValGlyPheThrIleGlyLeuLeuAlaArgArgPheLeuIleProProLeuIleVal 387
Db 948 GACATC-----TCCGACGTGATGATGCCAGGCGCTGTGATCCCGCGGATCTGTGTC 895
QY 388 AlaIleAlaGlyIleThrProMetLeuProGlyLeuAlaIleTygArgGlyMetTygAla 407
Db 894 CTC-----GGCGTGAACATCTCG----- 877
QY 408 ThrLeuAsnAspGlnThrLeu-----MetGlyPheThrAsnIleAla----- 421
Db 876 ACCACCAAGACAAACCGCGCTGTATGCTTCGCGCGCTGCGCGCGCGCGCGCGCG 817
QY 422 -----ValAlaLeuAlaThrAlaSerSerLeu----- 430
Db 816 TCCAGCGCGTTCCTGGCGATGTCACAGCGCGCGCGCGCGCGCGCGCGCGCGCG 757
QY 431 -----AlaAlaGly 433
Db 756 TACACCACTTCGTGGCGTGTGACCTTCCTCCGCGCGCGCGCGCGCGCGCGCGCG 697
QY 434 ValValLeuGlyGluTyrPheAlaAlaArgArgLeuArgArgProProArgPheAsnProTyr 453
Db 696 GTGATCATCGCGCATCTGATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 644
QY 454 ArgAlaPheThrIleValAlaAsnGluPheSerPheGlnGluGluAlaGluGlnAsnArg 473
Db 643 CGGCGACATCCA-----GGCGATCACTGGCGCGCGCGCGCGCGCGCGCGCG 599
QY 474 ---ArgGlnArgIleArgPro-----LysThrAsnGlnArgPheGlyValAsn 487
Db 598 CTGGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 539
QY 488 LysArg 489
Db 538 CGCGCG 533

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Search completed: July 31, 2004, 11:47:18  
 Job time : 4823 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 31, 2004, 10:08:48 ; Search time 585 Seconds

(without alignments)  
4098.522 Million cell updates/sec

Title: US-09-963-521-2  
Perfect score: 2432  
Sequence: 1 MMSFATLRGRISTVDAKAA.....QNGRGRKPKTNQRFGRNR 489

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
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-Q/cgn2\_1/USPTO.spool/p/US09963521/funat.27072004.114908.5693/app.query.fasta.1.647  
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-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100  
-THR.MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NOR=ext -HEADSIZE=500 -MINLEN=0  
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5  
-Fgapop=6 -Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
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12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/2/pubpna/US10D\_NEW\_PUB.seq:\*  
18: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
19: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

Result Query \*  
No. Score Match Length DB ID Description

1	2432	100.0	1503	9	US-09-738-626-2884	Sequence 2884, Ap
2	2432	100.0	1590	13	US-10-627-476-557	Sequence 557, Ap
3	2432	100.0	1590	13	US-10-450-055-41	Sequence 41, Ap
4	2432	100.0	1909	9	US-09-951-536-3	Sequence 3, Appl
5	2432	100.0	1909	9	US-09-963-521-3	Sequence 3, Appl
6	2432	100.0	1909	9	US-09-834-721-3	Sequence 3, Appl
7	2432	100.0	1909	9	US-09-783-388-3	Sequence 3, Appl
8	2432	100.0	1903	10	US-09-951-535-3	Sequence 3, Appl
9	2432	100.0	1909	17	US-10-924-574-11	Sequence 11, Appl
10	2432	100.0	2817	9	US-09-951-536-1	Sequence 1, Appl
11	2432	100.0	2817	9	US-09-963-521-1	Sequence 1, Appl
12	2432	100.0	2817	9	US-09-834-721-1	Sequence 1, Appl
13	2432	100.0	2817	9	US-09-783-388-1	Sequence 1, Appl
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15	2432	100.0	2817	17	US-10-924-574-9	Sequence 9, Appl
16	2432	100.0	3309400	9	US-09-738-626-1	Sequence 1, Appl
17	770	31.7	3010	14	US-10-058-945-1	Sequence 1, Appl
18	408	16.8	1659	15	US-10-156-761-4644	Sequence 4644, Ap
19	408	16.8	9025608	15	US-10-156-761-1	Sequence 1, Appl
20	230.5	9.5	9172	9	US-09-070-927A-65	Sequence 65, Appl
21	196.5	8.1	3632	16	US-10-398-221-3672	Sequence 3672, Ap
22	190	7.8	9834	8	US-08-781-986A-37	Sequence 37, Appl
23	190	7.8	9834	13	US-10-329-624-37	Sequence 37, Appl
24	188.5	7.8	1163020	16	US-10-398-221-10	Sequence 10, Appl
25	188.5	7.8	3011208	16	US-10-398-221-187	Sequence 2058, Ap
26	178.5	7.3	2594	9	US-09-070-927A-187	Sequence 187, Ap
27	175.5	7.2	2731748	17	US-10-297-465A-1	Sequence 1, Appl
28	169.5	7.0	18436	13	US-10-158-844-87	Sequence 87, Appl
29	165	6.8	23210	13	US-10-672-787-17	Sequence 17, Appl
30	147.5	6.1	1266	13	US-10-282-122A-1916	Sequence 14916, A
31	147.5	6.1	12278	16	US-10-398-221-3886	Sequence 3886, Ap
32	147	6.0	9219	16	US-10-282-122A-12963	Sequence 12963, A
33	144.5	5.9	3309400	9	US-09-738-626-1	Sequence 1, Appl
34	143.5	5.9	63158	15	US-10-292-198-1	Sequence 1, Appl
35	143	5.9	1230	13	US-10-282-122A-41648	Sequence 41648, A
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39	137.5	5.7	1854	16	US-10-398-221-1040	Sequence 1040, Ap
40	137.5	5.7	1854	16	US-10-398-221-2857	Sequence 2857, Ap
41	136	5.6	1863	13	US-10-282-122A-38255	Sequence 38255, Ap
42	134.5	5.5	1647	15	US-10-156-761-6431	Sequence 6431, Ap
43	134.5	5.5	2112	15	US-10-156-761-3675	Sequence 3675, Ap
44	134.5	5.5	2731748	17	US-10-297-465A-1	Sequence 1, Appl
45	134	5.5	1128	9	US-09-738-626-2689	Sequence 2689, Ap

## ALIGNMENTS

RESULT 1  
US-09-738-626-2884  
; Sequence 2884, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIO  
; APPLICANT: OCHIAI, KETKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAOKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OR INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738, 626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: JP 00/28098  
 PRIOR FILING DATE: 2000-08-03  
 NUMBER OF SEQ ID NOS: 7059  
 SOFTWARE: PatentIn ver. 3.0  
 SEQ ID NO: 2884  
 LENGTH: 1503  
 TYPE: DNA  
 ORGANISM: *Corynebacterium glutamicum*  
 US-09-738-626-2884

Alignment Scores:

Pred. No.:	1,18e-263	Length:	1503
Score:	2432.00	Matches:	489
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0

US-09-963-521-2 (1-489) x US-09-738-626-2884 (1-1503)

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Db	37	ATGTTGAATTTTGGCAACCTTCGTGGCCGCAATTCACAAGTTGACGGTGCAGAAAGCCGCA	96
QY	21	ProProSerSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAglVal	40
Db	97	CCTCGGCCATGCCCACTAGCCCCCATTTATCTCACTGACCATATGTCCAAGTGGCCGGTGTG	156
QY	41	MetAsnLeuAlaAlaArgLLeuAspLLeuLeuSerSerGlyThrSerIasnSerAsp	60
Db	157	ATGAATTTGGCTGCAGAAATGGCCATATTTTGCTTTCTTCAGGTACGCAAAATGTGAC	216
QY	61	ThrIysValGlnValArgAlaValThrSerAlaTyrGlyLeuTyrTyrHisValAsp	80
Db	217	ACCAAGGTACAGTTCCAGACGTGACCTTGGCTAGCGTTTGTACTACACGACGCGGAT	276
QY	81	IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGlnArgLysMetProVal	100
Db	277	ATCAAGTTGAATACGATCACCATCTTCACCAACATCGGTGGAGAGAAAGATCCGGTC	336
QY	101	AsnValPheHisValValGlyLysLeuAspThrAsnPhseSerLysLeuSerGluValAsp	120
Db	337	AACGGTTTCAGTTGTAGTGAAGTGGACACCAACTTCCAAACTGCTGTGAGTTGAC	396
QY	121	ArgLeuIleArgSerIleGlnAlaGlyAlaThrProGluValAlaGlnLysIleLeu	140
Db	397	CGTTTGATCCGTTCCATTCAGGCTGTGGGACCCCGCTGAGGTTGCCAGAAATCTCTG	456
QY	141	AspGluLeuGlnGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyTyrPala	160
Db	457	GACGAGTTGGAGCAATCCCTGGGTCTTATGTGTTCCCTGTGCTGTGCTGGGCA	516
QY	161	MetMetGlyGlyAlaValAlaValLeuLeuGlyGlyGlyTyrGlnAlaSerLeuIleAla	180
Db	517	ATGATGGGTGGTGGCTGTCTGTGCTGTGGGTGGGTGAAGGAGGATTTCCCTAAATGCT	576
QY	181	PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyLysIysGlyLeuPro	200
Db	577	TTTATTAACCGCGTTCCAGATCATTTGCCACAGCTCATTTTGGGAAAGAGGTTTGCT	636
QY	201	ThrPhePheGlnAsnValValGlyGlyPheIleAlaThrIleuProAlaSerIleAlaTyr	220
Db	637	ACTTCTTCCAAATATGTTGTGTGTATTTATTTGACACGCTGCCTGCATGATGTGTTAT	696
QY	221	SerLeuAlaLeuGlnPheGlyLeuGluIleLysProSerGlnIleIleAlaSerGlyIle	240
Db	697	TCTTTGGCGTGGCAATTTGGTCTTTGAGATAAACCGAGCCAGATCATCGATCTGGAAT	756
QY	241	ValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyAla	260
Db	757	GTTTGCTGTGGCAGGTTTGAACATCTGTGCATATCTGCAGACGGCATCACGGGGCT	816
QY	261	ProValThrAlaSerAlaArgPhePheGluThrLeuLeuPheThrGlyIleValAla	280

Db	817	CCGGTACAGCAAGTGCACGATTTTTCGAACACCTCTGTTTACCGCGGCATTTGTTGCT	876
QY	281	GLYVALGLYLEUGLYLLEGLINLEUSERGILULENHISVALMETLEUPROLAMETGLU	300
Db	877	GGCGTGGGTTTGGGCAATTCAGCTTTCTGAAATCTTCATCTCAWTTGGCTGCGCATGGAG	936
QY	301	SEVALALALAPROBENLYRSESERDHPHESALARGILEILELAGLYVALTHIR	320
Db	937	TCCGTGCACACCTATATTATGTGTCACTTGCACATTCGCCGCAATTTCGTGTGGCGTCACC	996
QY	321	ALALALALAPHEALVALGLCYSTRVALAGLUTPSESERVALILEILELAGLYLEU	340
Db	997	GCAGCGGCGCTTCGACAGTGGTTGTTACGCCGAGGTGGCTCGGTGATTATTGGCGGGCTT	1056
QY	341	THRALALEUMETGLYSERIALAPHELYRTTYLEUPHEVALVALTYLEUGLYPROVALSER	360
Db	1057	ACTGCGCTGATGGGCTTCGGCTTTTATTACCTCTGTTGTTATTTAGGCCCGCTCTCT	1116
QY	361	ALALALALILEALALATHRALVALVALGLYPHEPTHGLYGLYLEUENALALARGARPE	380
Db	1117	GCCGCTCGCATTTGCTGCACACGACGAGTTGTTCACTGCTGTTTGCCTTGCCTGCCGATTC	1176
QY	381	LEULLEPROFROLEULLEVALALALILELAGLYLLETHRPROCTLEUPROGLYLEUALA	400
Db	1177	TTGATTTCCACCGTTGATTGTGGCATTCGCCGATTCACACCAATGCTTCCAGGCTTAGCA	1236
QY	401	ILELYTRARGLYMETTYRALATHRLEUASASPDLINTHRLEUMETGLYPETHRASILE	420
Db	1237	ATTTCACCGCGAATGTACGCCACCTTAAGATTAACAACCTCATGGTTTCCACCAATTT	1296
QY	421	ALAVALALAEUALATHRALASERSEULEUALALAGLYVALVALLEUGLYLUTPIL	440
Db	1297	GCGGTTGCTTTAGCCATCTGCTTCATCACTTGCCGCTGGCGTGGTTTGGGTGGATTC	1356
QY	441	ALALARGTGLEUALARGPROPARGPHASAPPROTYRARGALAPETHRILYSALASN	460
Db	1357	GCCGCGACGGCTACGTGTGCCACCGCTTCAACCCCAATCCGTGCATTTACCAAGCGAAT	1416
QY	461	GLUPHESERPHEGLINGLUALAGLUGLNASGLNARGARGINARGLYSARGPROLYS	480
Db	1417	GAGTTCTCTCCACGAGGAAAGCTGACACGATCAGCGCGGCGAGAAACGTCCTCAAG	1476
QY	481	THRASGLNARGPHEGLYASHLYSARG	489
Db	1477	ACTAATCAAGATTCGGTAATMAAAG	1503
RESULT 2			
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/ Sequence 557, Application US/10627476			
/ Publication No. US20040030116A1			
GENERAL INFORMATION:			
APPLICANT: Pompeius, Mark			
APPLICANT: Kroege, Burkhard			
APPLICANT: Schoder, Hartwig			
APPLICANT: Zeider, Oskar			
APPLICANT: Haberhauser, Gregor			
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS			
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE			
FILE REFERENCE: BGI-125CPN			
CURRENT APPLICATION NUMBER: US/10/627,476			
CURRENT FILING DATE: 2003-07-25			
PRIOR APPLICATION NUMBER: 09/602,787			
PRIOR FILING DATE: 2000-06-23			
PRIOR APPLICATION NUMBER: USSN 60/141031			
PRIOR FILING DATE: 1999-06-25			
PRIOR APPLICATION NUMBER: DE 19931454.3			
PRIOR FILING DATE: 1999-07-08			
PRIOR APPLICATION NUMBER: DE 19931478.0			
PRIOR FILING DATE: 1999-07-08			
PRIOR APPLICATION NUMBER: DE 19931563.9			
PRIOR FILING DATE: 1999-07-08			

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; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 557
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1567)
; OTHER INFORMATION: RXN00349
US-10-627-476-557

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## Alignment Scores:

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Pred. No.:      1,296-263      Length:      1590
Score:           2432.00      Matches:      489
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:               13           Gaps:           0

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US-09-963-521-2 (1-489) x US-10-627-476-557 (1-1590)

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QY      21 PropProSerProleuAlaProIIeaPleuThrAspHisSerGluValaIagIVal
DB      161 CCTCCGCCATCGCCACTAGCCCGGATGATCTCAAGCAATGTAAGTGGCGGTGTG
        220

QY      41 MetAsnIeuAlaAlaArgIIeGlyAspIIeLeuIeuSerSerGlyThrSerAsnSerAsp
DB      221 ATGAAATTTGGCTGCGGAATTTGGCGAATTTTGGCTTCTTCAGTACGTCGAATAGTGAC
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QY      61 ThrIuValGluValaIArgAlaValaThrSerAlaTyrgIyLeuTyrrTyrrHisValaAsp
DB      281 ACCAAGATCAAGATTGACAGTGAACCTCTGCGTACGTTGTGACTACACGACGCGAT
        340

QY      81 IleThrIeuAsnThrIleThrIlePheThrAsnIIeGlyValGluArgIyMetProVal
DB      341 ATCAAGTTGAATACGATCAACATCTTCACCAACATCGGTGAGAGGAAGATGCCGCTC
        400

QY      101 AsnValaPheHisValaValaGlyIyLeuAspThrAsnPheSerIyLeuSerGluValaAsp
DB      401 AACGATTCTCATGTTGTAGCAAGTTGACACCAATTTCTCCAACTGCTTGAGTTGAC
        460

QY      121 ArgIeuIIeaArgSerIIeGluIIaGlyAlaThrProProGluValaIaGluIySIIeIeu
DB      461 CGTTTGATCCGTTCAATTCAGCTGCTGTCGACCCCGCTGAGGTGCCGAAATCTCG
        520

QY      141 AspGluIeuGluGluSerProIaSerTyrgIyPheProValAlaIeuIeuIyTrpAla
DB      521 GACGAGTTGAGCAATCCCTCGCTTATGAGTTTCCCTGTCGTTGCTTGGCTGGGA
        580

QY      161 MetMetGlyGlyValaValaIaValaIeuIeuGlyIyTrpGluValaSerIeuIIea
DB      581 ATGATGGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
        640

QY      181 PheIleThrAlaPheThrIleIleIleAlaThrThrSerPheIeuGlyIySIIeIeuPro
DB      641 TTATATACCGGCTTCAAGATCAATTCACGAGATATTTTGGGAAAGAGGATTTGCT
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QY      201 ThrPhePheGluAsnValaValaGlyIyPheIleAlaThrIeuProIaSerIleAlaTyrr
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DB      701 ACTTCTTCCAAATATGTTGGTGGTTTATGCGACGCTGCTGATGATTCCTAT
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QY      221 SerIeuAlaIeuGluPheGlyIyLeuGluIIeIyPheProSerGluIIeIleAlaSerGlyIy
DB      761 TCTTGGCGGTTGAATTTGGTCTTGAGATCAAAACCGGACCAATCATCGCATCTGGAAAT
        820

QY      241 ValValIeuIeuAlaGlyIeuThrIeuValaGIIeSerIeuGluAspGlyIyIleThrGlyVala
DB      821 GTTGTGCTGTTGGCAGGTTTGAACATCTGCAATCTTGCAGAGACGCGCATTCAGGCGCT
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QY      261 ProValThrAlaSerAlaArgPhePheGluThrIeuIeuPheThrGlyIyIleValaIa
DB      881 CCGGTACAGCAGATGACGATTTTCGAAACCTCGTTTACCGCGGCGCATTTGCT
        940

QY      281 GlyValGlyIeuGlyIyIleGluIeuSerGluIIeIeuHisValaMetIeuProIaMetGlu
DB      941 GCGGTGGGTTGGGCAATTCAGCTTCTGAAATCTTCATGTCATGTTGCTGCTGCTGATGAG
        1000

QY      301 SerAlaAlaAlaProAsnTyrrSerSerThrPheAlaArgIleIleIleAlaGlyValaThr
DB      1001 TCCGCTGACAGCACTTAATTTGCTTACATTCGCCGCAATTCGCTGAGGCGTACC
        1060

QY      321 AlaAlaAlaPheAlaValaGlyCyrrAlaIagIuTrpSerSerValIleIleAlaGlyIeu
DB      1061 GCAGCGGCTTCGCAAGTGGTTGTACGCGAGTGTCTCGGTGATTTATTCGGGGCTT
        1120

QY      341 ThrAlaIeuMetGlySerAlaPheTyrrTyrrIeuPheValaTyrrIeuGlyProValSer
DB      1121 ACTGCGCTGATGGGTTGCTGCTGTTTATACCTCTTGTGTTTATTTAGGCCCGGCTCTCT
        1180

QY      361 AlaAlaAlaIleAlaAlaThrAlaValaGlyPheThrGlyIyLeuIeuAlaArgPhe
DB      1181 GCGGTGCTTTCGCAACAGAGTGTTCACGCGGTGCTTCCGCTGCTGCTGCTGCTGCTGCT
        1240

QY      381 IeuIleProProIeuIleValaAlaIleAlaGlyIleThrProMetIeuProGlyIeuAla
DB      1241 TTGATTCACCGCTGATGTTGGGATGCGGATGCGGATGCAACCAATGCTTCAGGTCTAGCA
        1300

QY      401 IleTyrrArgGlyMetTyrrAlaThrIeuAsnAspGluThrIeuMetGlyPheThrAsnIle
DB      1301 ATTTCAGGGAATGACCCGACCTCGAATGATCAACCACTAGTGGTTTCACCAACAT
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QY      421 AlaValaIaIeuAlaThrAlaSerSerIeuAlaAlaGlyValaValaIeuGlyIuTrpIle
DB      1361 GCGGTGCTTTCGCAACAGAGTGTTCACGCGGTGCTTCCGCTGCTGCTGCTGCTGCTGCT
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QY      441 AlaArgAlaGluIeuArgProProAlaArgPheAsnProTyrrAlaIaPheThrIyAlaAsn
DB      1421 GCCCGAGGCTACGTCGTCACACGCTTCAACCAATACGTCATTTACCAAGCGGAAT
        1480

QY      461 GluPheSerPheGluGluGluIaGluGluIaGluIaGluIaGluIaGluIaGluIaGluIa
DB      1481 GAGTCTCTCTTCCAGAGAGAGCTGACGAATACGCGCGGAGAGAGAGAGAGAGAGAGAG
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QY      481 ThrAsnGluArgPheGlyAsnIySArg
DB      1541 ACTAATTCAGAAATTCGTTATTAAGG
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RESULT 3
US-10-450-055-41
; Sequence 41, Application US/10450055
; Publication No. US20040043953A1
; GENERAL INFORMATION:
; APPLICANT: BASF Aktiengesellschaft
; TITLE OF INVENTION: No. US20040043953A1el genes of Corynebacterium
; FILE REFERENCE: 936.2000
; CURRENT APPLICATION NUMBER: US/10/450.055
; CURRENT FILING DATE: 2003-06-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 41
; LENGTH: 1590

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TYPE: DNA  
 ORGANISM: Corynebacterium glutamicum  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (101)..(1567)  
 OTHER INFORMATION: RXS00349  
 US-10-450-055-41

## Alignment Scores:

Pred. No.:	1,29e-263	Length:	1590
Score:	2432.00	Matches:	489
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-09-963-521-2 (1-489) x US-10-450-055-41 (1-1590)

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QY      1 MetLeuSerPheAlaThrLeuAArgIleSerThrValAspAlaIaIaIa 20
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QY      21 ProProSerProLeuAlaProIleAspLeuThrAspHisSerGlnValaIaIa 40
DB      161 CCTCCGCCATGCGCATTAGCTCACTGACCAATGATCAAGTGGCCGCTGTG 220
QY      41 MetAsnLeuAlaIaArgIleAspIleLeuLeuSerGlyThrSerAsnSerAsp 60
DB      221 ATGAAATTTGGCTGGCAAAATTTGGCATTTTCTTTCAGGTACGTCAAAATAGTGAC 280
QY      61 ThrIleValGlnValaArgAlaValaThrSerAlaIleValIleValIleVal 80
DB      281 ACCAAGGTACAAAGTTCAGCAGTGCCTCTGCGTACGGTTGATCAACGACGACGTGAT 340
QY      81 IleThrLeuSerThrIleThrIlePheThrAsnIleGlyValaGluArgLysMetProVal 100
DB      341 ATCAGTTGAATAGATACCATCTTCAACCAATCGGTGGAGAGAAATCCGGTC 400
QY      101 AsnValPheHisValaIaGlyIleAspThrAsnPheSerIleLeuSerGlyValaIaIa 120
DB      401 AACGTGTTTCAATGTTGATGAGCAAGTGGACACCAACTCTCCAAATGTTGAGAGTTGAC 460
QY      121 ArgLeuIleAspSerIleGlnAlaGlyAlaThrProProGlnValaIaGluIleValIle 140
DB      461 CGTTTGATCCCTTCATTCAGCTGCTGCGACCCCGCTGAGGTGGCCGAAATAATCTGTG 520
QY      141 AspGluLeuGlnGlnSerProAlaSerIleGlyPheProValaIaLeuLeuGlyTyrAla 160
DB      521 GACGAGTTGGAGCAATCCCTGCGCTTATGTTTCCCTGTGCTGCTGGCTGGCA 580
QY      161 MetMetGlyGlyAlaValaIaValLeuLeuGlyIleGlyTyrPGLValaIaIaIa 180
DB      581 ATGATGGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 640
QY      181 PheIleThrAlaPheThrIleIleIleIleIleIleIleIleIleIleIleIleIle 200
DB      641 TTTATACCGGTTCACATCATTCGCAAGCATTTTGGAGAAAGAGGTTGCT 700
QY      201 ThrPhePheGlnAsnValaIaGlyIlePheIleIleIleIleIleIleIleIleIleIle 220
DB      701 ACTTTCTTCCAAAATGTTGTTGTTGTTTATGTCACGCTGCTGCTGCTGCTGCT 760
QY      221 SerLeuAlaLeuGlnPheGlyLeuGlnIleLysProSerGlnIleIleIleIleIle 240
DB      761 TCTTTGGCGTTGCAATTTGCTTGAATCAAAACCGAGCAAGATATGCAATCTGAAAT 820
QY      241 ValValIleLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyAla 260
DB      821 GTTGGCTGTTGGCGAGGTTTACACTCGGCAATCTGCAAGAGACGCAATCCGGGCGCT 880
QY      261 ProValThrAlaSerAlaArgPhePheGlnThrLeuLeuPheThrGlyIleValaIa 280
DB      881 CCGGAGACGAGAGTGAAGATTTTTCGAAACATCTCTGTTTACCGGGCGGCAATGTGCT 940

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QY      281 GlyValGlyLeuGlyIleGlnLeuSerGlnIleLeuHisValMetLeuProAlaMetGlu 300
DB      941 GGGGTGGGTTTGGGCAATGAGCTTCTGAAATCTTGCAATCTATGCTGCTGCTGCAAGAG 1000
QY      301 SerAlaAlaIaProAsnIleSerSerThrPheAlaArgIleIleAlaGlyIleValaIa 320
DB      1001 TCCGCTGCAAGCACTTATATTTGTTTACATTCGCGGCAATTCGCTGCTGCTGCTGCT 1060
QY      321 AlaAlaIaPheAlaValaIaGlyCysIleValaGluIleIleIleIleIleIleIleIle 340
DB      1061 GCAGCGGCTTCCGAGTGGGTTGTACGCGAGTGTGCTCGGATGATTTGCGGGCTT 1120
QY      341 ThrAlaLeuMetGlySerAlaPheIleIleIleIleIleIleIleIleIleIleIleIle 360
DB      1121 ACTGCGTGAATGAGCTTCTGCTTTTATTTACTCTTCTGCTTTTATTTAGCCCGGCTCT 1180
QY      361 AlaAlaAlaIleAlaIaThrAlaValaIaGlyPheThrGlyIleLeuAlaIaArgIlePhe 380
DB      1181 GCGGCTGCGATTCCTGCAACAGCAGTTGGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCT 1240
QY      381 LeuIleProProLeuIleValaIaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400
DB      1241 TTGATTCACCGTTGATTTGGCGATTCGCGGATACACCAATGCTTCCAGGCTTACCA 1300
QY      401 IleTyrArgIleMetTyrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle 420
DB      1301 ATTTACCGCGAATGTCAGCCCACTTGAATCAATCACTCACTGCTGCTGCTGCTGCTGCT 1360
QY      421 AlaValaIaLeuAlaThrAlaSerSerLeuAlaIaGlyValaIaLeuGlyIleValIle 440
DB      1361 GCGGTTGCTTTAGCACTGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1420
QY      441 AlaArgArgLeuArgArgProProArgPheAsnProIleValaIaPheThrIleValaIa 460
DB      1421 GCCCGCAGGCTACCTGCTTCAACAGCTTCAACCAATCGGTGATTTTACCAAGCGAAT 1480
QY      461 GluPheSerPheGlnGlnGlnIleAlaGlyIleAsnGlnArgGlnArgIleValaIa 480
DB      1481 GAGTTTCTCTTCCAGAGGAAAGTGAACAGATAGCGCGGAGAGAAACGTCCTCAAG 1540
QY      481 ThrAsnGlnArgPheGlyAsnIleArg 489
DB      1541 ACTAATCAGAGATTCGGTAAATAAAGG 1567

```

## RESULT 4

US-09-951-536-3

Sequence 3, Application US/09951536

Patent No. US20020107378A1

GENERAL INFORMATION:

APPLICANT: ZIEGLER, PETRA

APPLICANT: EGGELENG, IOTHAIR

APPLICANT: SAHM, HERMANN

APPLICANT: THIERBACH, GEORG

TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND

TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE

TITLE OF INVENTION: USING CORNEFORM BACTERIA

FILE REFERENCE: 21123/282414/MAS

CURRENT APPLICATION NUMBER: US/09/951,536

CURRENT FILING DATE: 2001-09-14

PRIOR APPLICATION NUMBER: 09/431,099

PRIOR FILING DATE: 1999-11-01

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 1909

TYPE: DNA

ORGANISM: Corynebacterium glutamicum

FEATURE:

NAME/KEY: CDS

LOCATION: (280)..(1746)

OTHER INFORMATION: tnfE-Gen

US-09-951-536-3

## Alignment Scores:

Pred. No.: 1,71e-263 Length: 1909  
 Score: 2432.00 Matches: 489  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-963-521-2 (1-489) x US-09-951-536-3 (1-1909)

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QY 1 MetLeuSerPheAlaThrLeuArgGlyArgIleSerThrValAspAlaIleValAla 20
DB 280 ATGTTGATTTTGGACCCCTTCGCGCCGCAATTCACAGTTGACGCTGCAGAAAGCCGCA 339
QY 21 ProProPheSerProLeuAlaProIleAspLeuThrAspHisSergValAlaGlyVal 40
DB 340 CCGCCGCGACGCGACATGACCCCGATTTGATCTCAGTACCATAGTCAGAGCCCGGTTG 399
QY 41 MetAsnLeuAlaIleArgIleGlyAspIleLeuLeuSerSergIleThrSerAsnSerAsp 60
DB 400 ATGAAATTTGGCTGCGGAATTTGGCATATTTGCTTCTTCAGGTACGTCAATAGTGAC 459
QY 61 ThrIleValGlnValArgAlaValIleThrSerAlaThrGlyLeuIleTyrThrHisValAsp 80
DB 460 ACCAAGGTACAAATTCAGACAGTACCTCTGCGTACGGTTTGATCAACGACGCGTGAAT 519
QY 81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGlnArgIleSmetProVal 100
DB 520 ATCAGCTTGAATGACATGACATCCATCTTCACCAATCGGTGTGAGAGAGAGATGCGGTC 579
QY 101 AsnValPheHisValValGlyIleLeuAspThrAsnPheSeriIleSergIleValAsp 120
DB 580 AACGTGTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAACTGTGAGGTTGAC 639
QY 121 ArgLeuIleArgSeriIleGlnIleGlyAlaThrProProGlnValAlaGlnIleSileu 140
DB 640 CATTGATCCGTTCCATTCAGGCTGTGTGCGACCCCGCTGAGGTTGCCAGAAATCCCG 699
QY 141 AspGlnLeuGlnIleSerProAlaSeriIleGlyPheProValAlaIleLeuGlyIleTPAla 160
DB 700 GACGAGTTGGACGACATCCCTCGCTTATGTTTCCCTGTCGTTGCTTGGCTGGGCA 759
QY 161 MetMetGlyGlyAlaValAlaValLeuLeuGlyIleGlyIleTyrGlnValSeriLeuIleAla 180
DB 760 ATGATGGGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 819
QY 181 PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyIleSergIlePro 200
DB 820 TTATATTCGCGCTTCAGATCAGATCAGTGCAGAGCTCATTTTGTGAAAGAGGATTTGCT 879
QY 201 ThrPhePheGlnAsnValValGlyIlePheIleAlaThrLeuProAlaSeriIleAlaTyr 220
DB 880 ACTTCTTCGAAATGTTGTTGTTGTTGTTTATTCGACAGCTGCTGCTGCTGCTGCTGCT 939
QY 221 SerLeuAlaIleGlnPheGlyLeuGlnIleIlePheSergIleIleAlaSergIleIle 240
DB 940 TCTTGGCGGTGCAATTTGCTTGAAGTCAACCGAGCGACATCATCTGCAATCTGGAAT 999
QY 241 ValValLeuLeuAlaGlyLeuThrLeuValGlnSeriLeuGlnAspGlyIleThrGlyAla 260
DB 1000 GTTGGCTGCTTGGACGTTGACATCTGTCGCAATCTTCGACGAGAGCGGCAATCGGCGCT 1059
QY 261 ProValThrAlaSerAlaArgPhePheGlnThrLeuLeuPheThrGlyIleValAla 280
DB 1060 CCGGAGCAGCAGAGTGCAGCATTTTTCGAAACATCTGTTTACCGGGCGGATTTTCT 1119
QY 281 GlyValGlyLeuGlyIleGlnLeuSergIleIleLeuHisValMetLeuProAlaMetGln 300
DB 1120 GCGGTGGGTTGGGATTCAGCTTCTTCAAACTTGATGTCATGTCATTTCCCTGCGCATGAG 1179
QY 301 SerAlaAlaAlaProAsnTyrSerSerThrPheAlaArgIleIleAlaGlyIleValThr 320
  
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DB 1180 TCGCTGCAGACCACTAATTAATTCGTACATTCGCCCGCATTAATTCGCTGGCGTACCC 1239
QY 321 AlaAlaAlaPheAlaValGlyCysTyrAlaGlnIleThrSerSerValIleIleAlaGlyLeu 340
DB 1240 GCAGCGGCTTCGCAAGGAGTGTACGCGAGTGTGCTCGGTGATTAATTTGGCGGCTT 1299
QY 341 ThrAlaLeuMetGlySeriAlaPheTyrTyrLeuPheValValIleIleGlyIleProValSer 360
DB 1300 ACTGCGCTGATGGGTTCTGCTGTTTATTAATCTTCTGCTGTTTATTAATTAATTAATTA 1359
QY 361 AlaAlaAlaIleAlaAlaThrAlaValAlaGlyPheThrGlyIleGlyLeuLeuAlaArgPhe 380
DB 1360 GCCGCTGACATTCGCTCAACAGCAGATGTTTCACTGATGATCACTATGAGGTTTACACCA 1419
QY 381 LeuIleProProIleIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400
DB 1420 TTGATTCACCGTTGATTTGTGGATTTGGCGGATCAACCAATGCTTCCAGGCTTACGA 1479
QY 401 IleTyrArgGlyMetTyrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle 420
DB 1480 ATTTACCGGGAATGTACCGCACTGATGATCACTATGAGGTTTACACCACTATGAGGTTT 1539
QY 421 AlaValAlaLeuAlaThrAlaSerSeriLeuAlaIleGlyValValLeuGlnIleTyrPhe 440
DB 1540 GCGGTGCTTTAGCCACTGCTTCATCATCTTGCCTGCGGTGGTGGTGGTGGTGGTGGT 1599
QY 441 AlaArgIleLeuArgProProArgPheAsnProTyrArgAlaPheThrIleValAsn 460
DB 1600 GCCCGAGGCTACGTGTCCACCGCTTCACCACTTACCGTGCATTTACCAAGGCGAAT 1659
QY 461 GluPheSerPheGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 480
DB 1660 GAGTTCTCTCTTCAGAGAGAACTGACAGCAATCAGCCGCGAGAGAAAGCTCCAAAG 1719
QY 481 ThrAsnGlnArgPheGlyAsnIleSarg 489
DB 1720 ACTAATCAGAGATTCGTTAATAAAG 1746
  
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## RESULT 5

```

US-09-963-521-3
Sequence 3, Application US/09963521
Patent No. US20020146781A1
GENERAL INFORMATION:
APPLICANT: ZIEGLER, PETRA
APPLICANT: EGGELING, LOTHAR
APPLICANT: SAHM, HERMANN
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE
TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF
FILE REFERENCE: 21123/282413/MAS
CURRENT APPLICATION NUMBER: US/09/963,521
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/431,099
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: DE 199 41 478.5
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1909
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (280)..(1746)
OTHER INFORMATION: thrE-gen
US-09-963-521-3
  
```

Alignment Scores:  
 Pred. No.: 1,71e-263 Length: 1909  
 Score: 2432.00 Matches: 489  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-963-521-2 (1-489) x US-09-963-521-3 (1-1909)

```

QY 1 MetLeuSerPheAlaThrLeuArgGlyArgGlyLeSerThrValAspAlaIalysAla 20
DB 280 ATGTTGAAGTTTGGCAACCTTCGTGGCCGCAATTCACAGCTTACCGCTGCAAAAGCCGCA 339
QY 21 ProProPseSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal 40
DB 340 CCCCCCGACATCCGACATCCGATTCATCAGCAGCATAGTCAAGTGGCCGGGTGTC 399
QY 41 MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp 60
DB 400 ATGAATTTGGCTCGAGAAATTTGGCGAATTTGCTTCTTCAGGTACGTCAAAATAGTGAC 459
QY 61 ThrIleValGlnValArgAlaValThrSerAlaTyGlyLeuTyThrHisValAsp 80
DB 460 ACCAAGGTACAGATTCAGAGAGTACCTTCGCTACGCTTGTGACAGCAGCGATGAT 519
QY 81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGlnArgIleMetProVal 100
DB 520 ATCAGCTTGAATGATGATCACCATCTTCACCAACATCGGTGGAGAGAGATGCCGATC 579
QY 101 AsnValPheHisValValGlyIleLeuAspThrAsnPheSerIleLeuSerGlnValAsp 120
DB 580 AACGTTTTCATGTTGAGGCAAGTTGGACACCAACTTCTCCAAACTGCTCGAGGTGAC 639
QY 121 ArgLeuIleArgSerIleGlnAlaGlyAlaThrProGlnValAlaGlnIleLeu 140
DB 640 CGTTTGAATCCGTTTCATTCAGGCTGGTGCGAACCCGCTGAGTTGCCGAGAAATCTCTG 699
QY 141 AspGlnLeuGlnGlnSerProIleAspTyGlyPheProValAlaLeuLeuGlyTyrAla 160
DB 700 GACGAGTTGAGGACATCCCTGCGCTTATAGTTTCCCTGTTGCTTGGCTGGCGCA 759
QY 161 MetMetGlyGlyAlaValAlaValLeuLeuGlyIleGlyTyrGlnValSerLeuIleAla 180
DB 760 ATGATGGGTGGTGTGCTGCTGCTGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 819
QY 181 PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyIleGlyValLeuPro 200
DB 820 TTTATTCACGGGTTTCAGATCATTTGCCACGACGATTTTGGGAAAGAGGTTTGCT 879
QY 201 ThrPhePheGlnAsnValAlaGlyIlePheIleAlaThrLeuProIleAlaTyr 220
DB 880 ACTTCTTCCAAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAT 939
QY 221 SerLeuAlaLeuGlnPheGlyLeuGlnIleLeuProSerGlnIleIleAlaSerGlyIle 240
DB 940 TCTTTGGCGTTGCAATTTGCTTGAATCAACCGAGCCAGATCATGCAATCTGGAAAT 999
QY 241 ValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyAla 260
DB 1000 GTTGTGCTGTGGAGAGTTTACACTGTGCAATCTTGGACAGCGGATCACGGGCGCT 1059
QY 261 ProValThrAlaSerAlaArgPhePheGlnThrLeuLeuPheThrGlyIleValAla 280
DB 1060 CCGGTGACAGCAAGTGACGATTTTTCGAAACACTCTGTTTACCGGGCGGATGTTGCT 1119
QY 281 GlyValGlyLeuGlyIleGlnLeuSerGlnIleLeuHisValMetLeuProIleMetGln 300
DB 1120 GGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 1179
QY 301 SerAlaAlaAlaProAsnTySerSerThrPheAlaArgIleIleAlaGlyValThr 320
DB 1180 TCCGCTGACAGCACTAATTTATTCCTACATTCGCCCGCATTAATGCTGGAGCGCTCAC 1239
QY 321 AlaAlaAlaPheAlaValAlaGlyCysTyrAlaGlnTyrSerSerValIleIleAlaGlyLeu 340
DB 1240 GCAGCGGCTTCGCGAGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1299

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QY 341 ThrAlaLeuMetGlySerAlaPheTyrTyrLeuPheValValTyrLeuGlyProValSer 360
DB 1300 ACTGGCTATGGGTTCCTGCGTTTATTAACCTTCTGTTGTTATTTAGGCCCGCTCTCT 1359
QY 361 AlaAlaAlaIleAlaAlaThrAlaValAlaGlyPheThrGlyIleLeuLeuAlaArgPhe 380
DB 1360 GCCGTGACATTCCTGCAACAGAGATGGTTCACAGGTGGTGTGTGTGTGTGTGTGTGTGTGT 1419
QY 381 LeuIleProProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400
DB 1420 TTGATTCACCGTGTGATGTTGGGATTTGCCGATTCACCAATGCTTCCAGSTCTAGCA 1479
QY 401 IleTyrArgGlyMetTyrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle 420
DB 1480 ATTTCACGGGATGATGACGCACTCGAATGATCAACATCACTAGGTTTCCACCAACAT 1539
QY 421 AlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValValLeuGlyIleTyrPle 440
DB 1540 GCGGTTGCTTTTACCCACTGCTTCATCATCTGCGCTGGCGTGTGTGTGTGTGTGTGTGTGT 1599
QY 441 AlaArgArgLeuArgArgProProArgPheAsnProTyrArgAlaPheThrIleAlaAsn 460
DB 1600 GCCCGAGGCTACGATGCTCCACACCGCTTACCCATACCGTGCATTTACCAAGCGCAAT 1659
QY 461 GluPheSerPheGlnGlnGlnAlaGlnGlnAsnGlnArgArgGlnArgIleGlySerProlys 480
DB 1660 GAGTTCTCTTCCAGAGGAACTGAGCAGATCAGCGCGGAGAGAGAAACGTCACAAAG 1719
QY 481 ThrAsnGlnArgPheGlyAsnIleArg 489
DB 1720 ACTAATCAGAGATTCGTAATTAATAAG 1746

```

RESULT 6

US-09-834-721-3

Sequence 3, Application US/09834721

Patent No. US2002015551A1

GENERAL INFORMATION:

APPLICANT: RIEBING, MECHTHILD

TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE

FILE REFERENCE: 21132/280169/MAS

CURRENT APPLICATION NUMBER: US/09/834,721

PRIOR FILING DATE: 2001-04-16

PRIOR APPLICATION NUMBER: DE 100 26 494.8

PRIOR FILING DATE: 2000-05-27

PRIOR APPLICATION NUMBER: DE 101 02 823.7

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3

LENGTH: 1909

TYPE: DNA

ORGANISM: Corynebacterium glutamicum

FEATURE:

OTHER INFORMATION: ATCC13032

NAME/KEY: CDS

LOCATION: (280)..(1746)

OTHER INFORMATION: thr gene

US-09-834-721-3

Alignment Scores:

Pred. No.: 1.71e-263 Length: 1909

Score: 2432.00 Matches: 489

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-963-521-2 (1-489) x US-09-834-721-3 (1-1909)

```

QY 1 MetLeuSerPheAlaThrLeuArgGlyArgGlyLeSerThrValAspAlaIalysAla 20
DB 280 ATGTTGAAGTTTGGCAACCTTCGTGGCCGCAATTCACAGCTTACCGCTGCAAAAGCCGCA 339

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QY 21 ProProSerProLeuAlaProIleAspLeuThrAspHisSerGluValAlaGlyVal 40  
 Db 340 CTTCCGCGCATTCGACATGCCCCGATTTGATCTTCACTGACATGATCAAGTGGCGGTG 399  
 QY 41 MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp 60  
 Db 400 ATGAATTTGGCTGGAGAAATTGGCGATATTGTTGCTTCTTCAAGTACGTAATATGATGAC 459  
 QY 61 ThrIleValGlnValAlaGlnAvalThrSerAlaTyrlGlyLeuTyrlThrHisValAsp 80  
 Db 460 ACCAAGGTACAGATTCAGAGAGTGAACCTTCGCTGACGTTGTACTACACGACAGTGGAT 519  
 QY 81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGluGlySerMetProVal 100  
 Db 520 ATACGTTGATATGATACATCACTTTCACCAACATGCGTGGAGAGAAATGCGCGTC 579  
 QY 101 AsnValPheHisValValGlyLysLeuAspThrAsnPheSerLysLeuSerGluValAsp 120  
 Db 580 AACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGAC 639  
 QY 121 ArgLeuIleArgSerIleGlnAlaGlyAlaThrProProGluValAlaGluLysIleLeu 140  
 Db 640 CGTTTATCCGTTCCATTCAGCGTGGCGACCCCGCTGAGGTTGCCAGAAATCTCTG 699  
 QY 141 AspGluLeuGluGlnSerProAlaSerTyrlGlyPheProValAlaLeuLeuGlyTyrPala 160  
 Db 700 GAGAGATTGGAGAAATCCCTGCGCTTATGTTTCCCTGTTGCGTGTGCTGGCTGGCA 759  
 QY 161 MetMetGlyValAlaValAlaValLeuLeuGlyGlyValTyrPalaSerLeuIleAla 180  
 Db 760 ATGATGGTGGTCTGTTGCTGTGCTGTGGGAGTGGAGAGGATTTCCCTAATGCT 819  
 QY 181 PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyLysIleGlyLeuPro 200  
 Db 820 TTTATTAACCGCTTCACGATCATTCGACACGCTCATTTTGGGAAGAAGGTTGGCT 879  
 QY 201 ThrPhePheGlnAsnValValGlyLysPheIleAlaThrLeuProAlaSerIleAlaTyrl 220  
 Db 880 ACTTTTCCAAATGTTGTTGGTGTATTAATGCGACGCTGCTGCATCGATTGCTTAT 939  
 QY 221 SerLeuAlaLeuGlnPheGlyLeuGluIleLysProSerGlnIleIleAlaSerGlyIle 240  
 Db 940 TCTTTGGCGTTGCAATTTGGTCTTGAGATCAACCGACGACATCTCCATCTGAAAT 999  
 QY 241 ValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyAla 260  
 Db 1000 GTTGGCTGTTGGAGTTGACACTCGGCAATCTCTCAAGACGCGCATCACGGCGCT 1059  
 QY 261 ProValThrAlaSerAlaPhePheGluThrLeuLeuPheThrGlyGlyIleValAla 280  
 Db 1060 CCGGTGACGCAAGTGCAGATTTTGCAGAACACTCTGTTTACCGCGCGCATTTGTTGCT 1119  
 QY 281 GlyValGlyLeuGlyIleGlnLeuSerGluIleLeuHisValMetLeuProAlaMetGlu 300  
 Db 1120 GCGGTGGGTTTGGCATTCAGCTTCTGAAATCTTGCAATGATATGTTGCTCCCATGGAG 1179  
 QY 301 SerAlaAlaAlaProAsnTyrlSerSerThrPheAlaArgIleIleAlaGlyValThr 320  
 Db 1180 TCCGCTGACGACCTTAATTAATTCGTCAATTCGCCCGCATTAATGCTGGTGGCTCAC 1239  
 QY 321 AlaAlaAlaPheAlaValGlyCysTyrlAlaGluTyrPheSerValIleIleAlaGlyLeu 340  
 Db 1240 GCAAGGCGCTTCGACGTGGGTTTACCGGAGAGTGTCTCGGATTAATGCGGCGCT 1299  
 QY 341 ThrAlaLeuMetGlySerAlaPheTyrlThrLeuPheValAlaTyrlLeuGlyProValSer 360  
 Db 1300 ACTGCGCATGAGGTTCTGCGTTTATTAACCTTCTGTTGTTATTTAGGCCCGCTCTCT 1359  
 QY 361 AlaAlaAlaIleAlaAlaThrAlaValGlyPheThrGlyGlyLeuLeuAlaArgArgPhe 380  
 Db 1360 GCGGTGGGATTTGCGCAACGACAGTGTGTTCACTGGTGGTTCCTGCGCGTGTGATTC 1419  
 QY 381 LeuIleProProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400

Db 1420 TTGATTCACCGTTGATTTGGGAGATTCGCGCATCACACCAATGCTTCCAGGCTTGCA 1479  
 QY 401 IleTyrArgGlyMetTyrlAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle 420  
 Db 1480 ATTTACCGCGAAATGTAAGCGCACCTCGAATGATCAACACTCATGAGGTTTCCACCAAT 1539  
 QY 421 AlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValValLeuGlyGluTyrIle 440  
 Db 1540 GCGGTGCTTTAGCCACTGCTTATCACTTCCGCGCTGGCTGGTGGTGGAGTGAAT 1599  
 QY 441 AlaArgArgLeuArgArgProProArgPheAsnProTyrlArgAlaPheThrLysAlaAsn 460  
 Db 1600 GCCCGCAGGCTACGTGTCACACGCTTCAACCAATACCGTGATTTACCAAGCGCAAT 1659  
 QY 461 GluPheSerPheGlnGluGluAlaGluGlnAsnGlnArgArgGlnArgGlySerProLys 480  
 Db 1660 GAGTTCTCTTCCAGAGAGAACTGAGCAAAATCAGCGCGCAGAAAAAGTCCAAAG 1719  
 QY 481 ThrAsnGlnArgPheGlyAsnLysArg 489  
 Db 1720 ACTAATCAGAGATTCCGTAATTAAGA 1746  
 RESULT 7  
 US-09-783-388-3  
 ; Sequence 3, Application US/09783388  
 ; Patent No. US20020168731A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ziegler, Petra  
 ; APPLICANT: Eggeling, Lothar  
 ; APPLICANT: Sahm, Hermann  
 ; APPLICANT: Thierbach, Georg  
 ; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND  
 ; TITLE OF INVENTION: PROCESS FOR  
 ; FILE REFERENCE: ENZYMATIC PRODUCTION OF L-THREONINE USING CORYNEFORM BACTERIA  
 ; CURRENT APPLICATION NUMBER: US/09/783,388  
 ; CURRENT FILING DATE: 2001-02-15  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1909  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium glutamicum ATCC13032  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (280)..(1746)  
 US-09-783-388-3  
 Alignment Scores:  
 Pred. No.: 1,716-263 Length: 1909  
 Score: 2432.00 Matches: 489  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0  
 US-09-963-521-2 (1-489) x US-09-783-388-3 (1-1909)  
 QY 1 MetLeuSerPheAlaThrLeuArgGlyArgIleSerThrValAspAlaAlaLysAlaAla 20  
 Db 280 ATGTGAGATTGTTGCGACACCTTCTGTGCGCATTTCAACAGTTGACGCTGCAGAAAGCGCGCA 339  
 QY 21 ProProSerProLeuAlaProIleAspLeuThrAspHisSerGluValAlaGlyVal 40  
 Db 340 CTTCCGCGCATTCGACATGCCCCGATTTGATCTTCACTGACATGATCAAGTGGCGGTG 399  
 QY 41 MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp 60  
 Db 400 ATGAATTTGGCTGGAGAAATTGGCGATATTGTTGCTTCTTCAAGTACGTAATATGATGAC 459  
 QY 61 ThrIleValGlnValAlaGlnAvalThrSerAlaTyrlGlyLeuTyrlThrHisValAsp 80



Db 460 ACCAAGGTAAGAATTGACAGTACCTCTGCGTTCGTTTACTACACGACCTGAT 519  
QY 81 ILeThLeuAsnThrIleThriIlePheThrAsnIleGlyValAlaGluArgLysMetProVal 100  
Db 520 ATCACTTGAATACGATACACATCTTACCAACATCGGTGTGAGAGAAATGCGGTC 579  
QY 101 AenValPheHisValValGlyLysLeuAspThrAsnPheSerLysLeuSerGlyValAsp 120  
Db 580 AACGTTTCATCTTGTAGGCAAGTGGACACCACTTCTCCAACTGCTGTGAGTTGAC 639  
QY 121 ArgLeuIleArgSerIleGlnAlaGlyAlaThrProGluValAlaGluLysIleLeu 140  
Db 640 CGTTTATCCGTTCCATTACGCTGTGCGACCCCGCTGAGGTTGCCGAGAAATCTCTG 699  
QY 141 AspGluLeuGluGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyTTPAla 160  
Db 700 GACGAGTTGAGCAATCCCTGCGCTTTATGTTGTTCCCTGTGCTTGCCTGGCGCA 759  
QY 161 MetMetGlyGlyAlaValAlaValLeuLeuGlyGlyLysTrpGlnValSerLeuIleAla 180  
Db 760 ATGATGGGTGGTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 819  
QY 181 PheIleThraIlePheThrIleIleAlaThrThrSerPheLeuGlyLysLysGlyLeuPro 200  
Db 820 TTTATTTACCGCTTACGATCATTTGCCACGACATTTTGGGAAAGAGGTTGCTCT 879  
QY 201 ThrPhePheGlnAsnValValGlyGlyPheIleAlaThrLeuProAlaSerIleAlaTyr 220  
Db 880 ACTTCTTCCAAATGTTGTGGTGTGTTTATTCACGCTGCTGCTGCTGCTGCTGCTAT 939  
QY 221 SerLeuAlaLeuGlnPheGlyLeuGlnLysProSerGlnIleIleAlaSerGlyIle 240  
Db 940 TCTTTGGCGTTGCAATTTGCTTGAATCAACCGACGATCATGCACTGCGAATT 999  
QY 241 ValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyAla 260  
Db 1000 GTTGTGCTGTTGCGAGTTTGACACTGCTGCAATCTGCGACGAGCGGATCACGGCGCT 1059  
QY 261 ProValThrAlaSerAlaArgPhePheGluThrLeuLeuPheThrGlyIleValAla 280  
Db 1060 CCGGTGACAGACGACGATTTTTCGAAACACTCCGTTTACCGCGGCGATTTGCTCT 1119  
QY 281 GlyValGlyLeuGlyIleGlnLeuSerGluIleLeuHisValMetLeuProAlaMetGlu 300  
Db 1120 GCGGTGGGTGGGATTCACCTTGTGAATCTTGCAATGTCATGTCCTGCGCATGAG 1179  
QY 301 SerAlaIleAlaProAsnTyrSerSerThrPheAlaArgIleIleAlaGlyValThr 320  
Db 1180 TCCGCTGACGACCTTAATTTTCGTCATTTCCGCGCATTTATGCGTGGCGTCAAC 1239  
QY 321 AlaAlaIlePheAlaValGlyCysTyrAlaGluTyrSerSerValIleIleAlaGlyLeu 340  
Db 1240 GCAGGCGCTTCGCGAGGTGTTGTTACCGCGAGTGTCTCGGTATTAATGCGGCGCTT 1299  
QY 341 ThrAlaLeuMetGlySerAlaPheTyrTyrLeuPheValValIyrLeuGlyProValSer 360  
Db 1300 ACTGGCGTGAATGGTTCGCGTTTATTAACCTTTCGTTTATTTAGGCCCCCTCTCT 1359  
QY 361 AlaAlaIleAlaIleAlaThrAlaValGlyPheThrGlyGlyLeuLeuAlaArgPhe 380  
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QY 381 LeuIleProProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400  
Db 1420 TTGATTTCCACCGTTATGTGTGCGATGTCGCGCATCACCAATGCTTCCAGGCTCAGA 1479  
QY 401 IleTyrArgGlyMetTyrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle 420  
Db 1480 ATTATCCGGGAAATGACGACCTCGAATGATCAAACTCATGGGTTTCCCAACATTT 1539  
QY 421 AlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValValLeuGlyLysTrpIle 440  
Db 1540 GGGGTGCTTTAGCCACTGCTTCATCACTTGCCTGCGGTGGTGGTTGGTGAAGTGAAT 1599

QY 441 AlaArgArgLeuArgArgProProArgPheAsnProTyrArgAlaPheThrIleAlaAsn 460  
Db 1600 GCCCGGAGGCTACGTCTGTCCACGACCTTCACCCCATACCTGTCATTTACCAAGGGAAT 1659  
QY 461 GluPheSerPheGlnGlnGlnAlaGlnGlnAsnGlnArgGlnGlnArgLysArgProLys 480  
Db 1660 GAGTCTCTCTTCCAGAGGAGAGCTGAGCAATACAGCGCGGAGAGAAACGTCACAAAG 1719  
QY 481 ThrAsnGlnArgPheGlyAsnLysArg 489  
Db 1720 ACTAATCAGAGATTGGTAATAAAG 1746  
RESULT 8  
US-09-951-535-3  
Sequence 3, Application US/09951535  
Publication No. US20030049802A1  
GENERAL INFORMATION:  
APPLICANT: ZIEGLER, PETRA  
APPLICANT: EGGELENG, LOTHAR  
APPLICANT: SAHM, HERMANN  
APPLICANT: THIERBACH, GEORG  
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND  
TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE  
FILE REFERENCE: 21123/282415/MAS  
CURRENT APPLICATION NUMBER: US/09/951,535  
PRIOR APPLICATION NUMBER: 09/431,099  
PRIOR FILING DATE: 1999-11-01  
PRIOR APPLICATION NUMBER: DE 199 41 478.5  
PRIOR FILING DATE: 1999-09-01  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 1909  
TYPE: DNA  
ORGANISM: Corynebacterium glutamicum  
FEATURES:  
NAME/KEY: CDS  
LOCATION: (280)..(1746)  
OTHER INFORMATION: thrS-Gen  
US-09-951-535-3  
Alignment Scores:  
Pred. No.: 1,71e-263 Length: 1909  
Score: 2432.00 Matches: 489  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
US-09-963-521-2 (1-489) x US-09-951-535-3 (1-1909)  
QY 1 MetLeuSerPheAlaThrLeuArgGlyValGlyIleSerThrValAlaAspAlaIleAla 20  
Db 280 ATGTTGAGTTTGGCAACCTTCGTGCGCATTTCAAGATTGACGCGCAAAACCGCA 339  
QY 21 ProProProSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal 40  
Db 340 CCTCGCATGCGCACGACGCCCATTAATCTCACTGACATGACATGACAGTGGCGGTGTG 399  
QY 41 MetLeuLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp 60  
Db 400 ATGATTTTGGCGGAGGATTTGGCATATTTGCTTCTTCAAGTACGTCANAATGTGAC 459  
QY 61 ThrLysValGlnValArgAlaValThrSerAlaTyrGlyLeuTyrTyrThrHisValAsp 80  
Db 460 ACCAAGTAAGAATTGACAGTACCTCTGCGTACGGTTTGTACTACACGACGATGAT 519  
QY 81 ILeThLeuAsnThrIleThriIlePheThrAsnIleGlyValAlaGluArgLysMetProVal 100  
Db 520 ATCACTTGAATACGATACACATCTTACCAACATCGGTGTGAGAGAAATGCGGTC 579



QY	101	AsnValPheHisValValGlyIleuAspThrAsnPhSerIleuSerGluValAsp	120
Db	580	AAcGTTCATGTTGAGGCAAGTTGGACCAACCACTTCACAACTGCTGAGGTTGAC	639
QY	121	ArgLeuIleArgSerIleGlnIleAGlyAlaThrProProGluValAlaGluIySIIleu	140
Db	640	CGTTGATCCGTTCCATTCAAGCGCTGGTGCACCCCGCTAGAGTTGCCGAAAAATCCTG	699
QY	141	AspGluLeuGluGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyIYrPalA	160
Db	700	GACGAGTTGAGCAATCCCTCGCGCTCTTAAGTTTCCCTGTTCGTTGCTGGCTGGCA	759
QY	161	MetMetGlyGlyIyAlaValAlaValLeuLeuGlyIyGlyIYrPglValSerLeuIleAla	180
Db	760	ATATAGGTGAGTGTGCTGTGCTGTGGTGGGAGGAGGAGGAGGATTTCCCAATTTGCT	819
QY	181	PheIleThrAlaPheThrIleIleAlaThrThSerPheLeuGlyIySlySglLeuPro	200
Db	820	TTTATTACCGCGTTCAAGATCATTTGACAGACGACTATTTTGGGAAAGAAAGGTTTGCT	879
QY	201	ThrPhePheGlnAsnValValGlyIyPheIleAlaThrLeuProAlaSerIleAlaYr	220
Db	880	ACTTCTTCCAAATCTGTGTGTATTATTCACACCTGCTGCATCGATTGCTAT	939
QY	221	SerLeuAlaLeuGlnPheGlyLeuGluIleIySProSerGlnIleIleAlaSerGlyIle	240
Db	940	TCTTTGGCGTTGCATTTTGCTTGAGATCAAAACGACGACATCATCGATCTGGAAT	999
QY	241	ValValLeuLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyAla	260
Db	1000	GTTTGCTGTGTGGCAGGTTTGACACTCGTGCAATCTCTCAAGACGGCATCAAGGGCGCT	105
QY	261	ProValThrAlaSerAlaPhePheGluThrLeuLeuPheThrGlyIyIleValAla	280
Db	1060	CCGGTGACGACGAAGTCCACGATTTTTCGAAACATCTCTGTTTACCGCGCGCATTTGCT	111
QY	281	GlyValGlyLeuGlyIYleGlnLeuSerGluIleLeuHisValMetLeuProAlaMetGlu	300
Db	1120	GCGCGGGGTTTGGGCAATTCAGCTTCTGAAACTTTCGATGTCATGTGCTCCATGGAG	117
QY	301	SerAlaAlaAlaProAsnIySerSerThrPheAlaArgIleIleAlaGlyIyAlaThr	320
Db	1180	TCCGCTGCACACCTTAATATTGCTACATTGCGCGCATTAATGCGTGGCGCTCAC	123
QY	321	AlaAlaAlaPheAlaValGlyCysTyrAlaGluIyPseSerValIleIleAlaGlyLeu	340
Db	1240	GCAGCGGCGCTTGGCAGTGGGTGTTAACGGGAGTGCTCTGGGTATTATTCGGGGCTT	129
QY	341	ThrAlaLeuMetGlySerAlaPheIyTyrIleuPheValTyrLeuGlyProValSer	360
Db	1300	ACTGGCGTGAAGGGTTCGCGTTTATTAACCTTCCTGTTGTTATTATTTAGGCCCCGCTCT	135
QY	361	AlaAlaAlaIleAlaAlaThrAlaValAlaGlyPheThrGlyIyLeuLeuAlaArgPhe	380
Db	1360	GCGCGTGCGATTGCGAACAGACATTTGGTTTCACTGTGTGTTTCTTCCCGCTGATTC	141
QY	381	LeuIleProProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla	400
Db	1420	TTGATTCCACCGTATATTGTGGCGATTCGCGGCATCAACCAATCTTCCAGGTCTACA	147
QY	401	IleTyrArgGlyMetTyrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle	420
Db	1480	ATTTACCGCGAATGTACGCCACCTGTATGATCAAAACATCAAGGATTCAACCAACT	153
QY	421	AlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValAlaLeuGlyIyIleTriPle	440
Db	1540	GCGGTGCTTTAGCACATGCTTCATCACTTCCCGCTGCGTGGTTTGGTGAAGATTT	159
QY	441	AlaArgAlaGlyLeuArgArgProProArgPheAsnProTyrArgAlaPheThrIyAlaAsn	460
Db	1600	GCCCGCAGGCTACGTCTGCCACAGCTTCAACCCATACCGTGAATTTTACCAAGCGCAAT	165

Qy		461	GluPheSerPheGlnGluValaIagLusInanSgInArArgClnmArgLysatGrProlys	480
Db		1660	GAGTTCTCCCTTCACGAGGAAGCTGGACGAATCACGCCCGCGACGAAACGTCCAAAG	1719
Qy		481	ThrAsnGlnArPheGlYAsnLysArg	489
Db		1720	ACTAATCAAGATTCGCTAATAAAGG	1746
			RESULT 9	
			US-10-224-574-11	
			/ Sequence 11, Application US/10224574	
			/ Publication No. US20040101837A1	
			GENERAL INFORMATION:	
			APPLICANT: Forschungszentrum Jlich GmbH; P. Ziegler, L. Eggeling, H. Sahm,	
			APPLICANT: P. Peters-Wendisch	
			TITLE OF INVENTION: Nucleotide sequences coding for proteins participating in the	
			TITLE OF INVENTION: L-Serin, improved process for the microbial manufacturing of L	
			TITLE OF INVENTION: genetically modified microorganism suitable for the process	
			FILE REFERENCE: PZT-9912-PCT	
			CURRENT APPLICATION NUMBER: US/10/224,574	
			CURRENT FILING DATE: 2002-08-21	
			NUMBER OF SEQ ID NOS: 12	
			SOFTWARE: Patentin Ver. 2.1.	
			SEQ ID NO: 11	
			LENGTH: 1909	
			TYPE: DNA	
			ORGANISM: C. glutanicum ATCC 13 032	
			FEATURE:	
			NAME/KEY: CDS	
			LOCATION: (280)..(1746)	
			OTHER INFORMATION: thr E (threonine-exportcarrier)	
			US-10-224-574-11	
			Alignment Scores:	
			Pred. No.: 1.71e-263	
			Score: 2432.00	
			Length: 1909	
			Matches: 489	
			Percent Similarity: 100.00%	
			Conservative: 0	
			Best Local Similarity: 100.00%	
			Mismatches: 0	
			Query Match: 100.00%	
			Indels: 0	
			DB: 17	
			Gaps: 0	
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Qy		1	MetLeuSerPheAlaThrLeuArgIYAArgIleSerThrValaAlaLysAlaala	20
Db		280	ATGTTGATTGTTGGACCCCTTGCTGGCCGCATTTCAACAGTTGACGTGCAAAAACCGCA	339
Qy		21	ProProSerProLeuAlaProIlLaSpLeuThrAspHLSerGlnValAlaLylVal	40
Db		340	CCTCCGCATGCCACCTAGCCCCCATGTCTCACTGACCATGTAAGTGCGCGTG	399
Qy		41	MetAsnLeuAlaAlaArgIleGIYAAspIleLeuLeuSerSerGIYThrSerAsnSerAsp	60
Db		400	ATGAATTGGCTGGACGAGATTGGCGAATTTGGCTTCTTAGAGTACGTCAAATAGTGAC	459
Qy		61	ThrIlystAlaGlnValaArgAlaValThSerAlaTyrgLyLeuTYrThHisValasp	80
Db		460	ACCAAGGTACAAGTTCCAGACAGTCACTCGCTGACGTTGTACTACACGCACTGGAT	519
Qy		81	IleThrLeuAsnThrIleThrIlePheThrAsnIleGIYAlaGluArgLysMetProVal	100
Db		520	ATCAGTTGATACGATACCATCTTCAACCAATGCGTGGAGAGAGAGATGCCGCTC	579
Qy		101	AsnValPheHisValaIalGIYLYsLeuAspThzAsnPheSerIlysLeuSerGIUValasp	120
Db		580	AACGTTGTCATGTTGTAGGCAAGTTGACACCACACTTCCAAAACGTCTGAAGTTGAC	639
Qy		121	ArgLeuIleArgSerIleGlnAlaGIYAlaThrProProGluValaIalGIYLYsIleLeu	140
Db		640	CGTTGATCGTTCCATTCAGGCTGGGCAACCCCGCTGAGGTGGCCGAAAAATCTTG	699
Qy		141	AspGluLeuGlnSerProAlaSerTYrGIYPheProValAlaLeuLeuGIYTrAla	160

Db	700	GACGAGTTGGACCAATCCCTCGCTTATAGTTTCCCTGGTGGCTTGGCTGGCGGCA	759
Qy	161	MeMeTcTgYyAlaVaAlaValleuLeuEngYgYlYTrpGlnVaSerIleuIleAla	180
Db	760	ATGATGGGGGTGGTGGTGGTGGTGGTGGGAGTGGATGGCAGGATTTCCCTAAATTGGCT	819
Qy	181	PhellleThrAlaPheThrIleIleAlaThrTrpSerPheLeuGlyLysIlysgYleuPro	200
Db	820	TTTATTACCGGCGTTCACGATCATGGCACAGACGTCAATTTTGGGAAAGAGGGTTTGCT	879
Qy	201	ThirPhepGlnAsnValAlGlyGlyPheIleAlaThrLeuProAlaSerIleAlaIYr	220
Db	880	ACTTTCTTCCAAATATGTTGGTGGTTTTATTTGCAACGGTGGCTGCATCGATTGGTAT	939
Qy	221	SerLeuAlaLeuGlnPheGlyLeuGluIleYsProSerGlnIleIleAlaSerGlyIle	240
Db	940	TCTTTGGCGTTGCATTTGATTTGCTTGGATCCAAACGAGCCAGATCATCGATCTGGAAAT	999
Qy	241	ValIValleuLeuAlaGlyLeuThrIleuValGlnSerLeuGlnAspGlyIleTrpGlyAla	260
Db	1000	GTTTGCGCTTTGGCAGAGTTTGAACATCGTCAAATCTCTGAGGAGGCGATCAGGGCGCT	1059
Qy	261	ProValThrAlaSerAlaIYrPhePheGluThrLeuLeuPheThrGlyIleValAla	280
Db	1060	CCGGTACACGAGTGCACGATTTTGGAAACGCTCGTTTACCGGCGGCAATGGTGGCT	1119
Qy	281	GlyValGlyLeuGlyIleGlnLeuSerGluIleLeuHisValMeTleuProAlaMeTlu	300
Db	1120	GGGCTGGGTTTGGCGATTCAGCTTTCTGAAATCTTGATCATGTTGCCCTGGCATAGAG	1179
Qy	301	SerAlaAlaAlaProAsnIYrSerSerThrPheAlaArgIleIleAlaGlyValThr	320
Db	1180	TCCGCTGACGACACTTATTTATGCTCAACATGGCCGCAATTCGCTGGTGGCGTACC	1239
Qy	321	AlaAlaAlaPheAlaValAlGlyCysYrAlaGluTrpSerSerValIleIleAlaGlyLeu	340
Db	1240	GCAGCGGCTTCCGACGTGGGTTGTACGCGGAGTGGTCTCGGATTAATGGCGGGCTT	1299
Qy	341	ThrAlaLeuMeTgYleSerAlaPheIYrYrLeuPheValIYrLeuGlyProValSer	360
Db	1300	ACTGCGGTGATGGGTTCTCGGTTTATTTACTCTTCTGTTTATTTAGGCGCCGCTCT	1359
Qy	361	AlaAlaAlaIleIleAlaThrAlaValAlGlyPheThrGlyGlyLeuAlaIaArgArPhe	380
Db	1360	GGCGCTGCGATTTGTGCAACGACGATTGGTTTCACTGGTGGTTTGGCCCGCTGATTC	1419
Qy	381	LeuIleProProLeuIleValAlaIleAlaGlyIleThrProMeTleuProGlyLeuAla	400
Db	1420	TTGATTCACCGTTGATTTGGGCGATTCGCGGATCAACCAAGCTTCCAGGCTAGCA	1479
Qy	401	IleYrArGlyMeTcYrAlaThrIleuAsnAspGlnThrIleuMeTgYlePheThrAsnIle	420
Db	1480	ATTTCACCGCGAATGTACGCGCACCTCATATCATCAACATCAATGGGTTTACCAAACTT	1539
Qy	421	AlaValAlaLeuAlaThrAlaSerSerIleuAlaIaGlyValIleuGlyGluTrpIle	440
Db	1540	GCGGTGCTTTAGCCACTGCTTCACTCACTTCCCGTGGCGTGGTTTGGTGAAGATTT	1599
Qy	441	AlaIaArgIleuArGArgProProArPheAsnProYrArGalIaPheThrIlyslAsn	460
Db	1600	GCCCGGACGACGTACGTCCGTCACCAACGCTTCAACCATATCGTGAATTTACCAAGCGCAAT	1659
Qy	461	GlnPheSerPheGlnGlnGluAlaGlnGlnAsnGlnIaArgGlnIaArgIlyArProLys	480
Db	1660	GAGTTCTCTCTCCGAGGAGGATCGAGCAGATCAGCGCGGACAGAGAAACGTCCAAAG	1719
Qy	481	ThrAsnGlnArgPheGlyAsnIlysArg 489	
Db	1720	ACTATACAGAGATTCGGTATATTAAGG 1746	

RESULT 10  
US-09-951-536-1  
; Sequence 1, Application US/09951536

Patent No. US20020107378A1  
GENERAL INFORMATION:  
APPLICANT: ZIEGLER, PETRA  
APPLICANT: EGGELING, LOTHAR  
APPLICANT: SAHM, HERMANN  
APPLICANT: THIERBACH, GEORG  
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND  
TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE  
TITLE OF INVENTION: USING CORNEFOM BACTERIA  
FILE REFERENCE: 21123/282414/MAS  
CURRENT APPLICATION NUMBER: US/09/951,536  
CURRENT FILING DATE: 2001-09-14  
PRIOR APPLICATION NUMBER: 09/431,099  
PRIOR FILING DATE: 1999-11-01  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 2817  
TYPE: DNA  
ORGANISM: *Corynebacterium glutamicum*  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (398)..(1864)  
OTHER INFORMATION: thrF-gen  
US-09-951-536-1

Alignment Scores:

Pred. No.:	3	136	253
Score:	2432.00		
Percent Similarity:	100.00%		
Best Local Similarity:	100.00%		
Query Match:	100.00%		
DB:	9		
		Length:	2817
		Matches:	489
		Conservative:	0
		Mismatches:	0
		Indels:	0
		Gaps:	0

US-09-963-521-2 (1-489) X US-09-951-536-1 (1-2817)

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QY	21	ProProProSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal	40
Db	458	CCTCCGCCATCGCCACTACGCCCGCATTTGATCTGACTGACCATATGCAAGTGGCCGGTGTG	517
QY	41	MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerIleSerAsp	60
Db	518	ATGAAATTGGCTGGCAGAAATGGCCGATTTTGGCTTCTTCAGGTACGTCACAAACAGTAGT	577
QY	61	ThrIysValGlnValArgAlaValThrSerAlaArgIleuLeuTyrThrHisValAsp	80
Db	578	ACCAAGGTCAGATTCGAGCGGTGACCTCTGGCATAGGCTGTACTATACGACATGGAGT	637
QY	81	IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGluArgLysMetProVal	100
Db	638	ATCAGCTTGAAATACGATCACCATTCTTCAACCAATCCGGGTGGAGAGGAAGATGCCGGTTC	697
QY	101	AsnValPheHisValValGlyLysLeuAspThrAsnPheSerLysLeuSerGluValAsp	120
Db	698	AACGCTTTCACTGTTGGTGGCAAGTTGGACACCAACTTCTCCAAATCGTCTGAGGTTGAC	757
QY	121	ArgLeuIleArgSerIleGlnAlaGlyAlaThrProProGluValAlaGluLysIleLeu	140
Db	758	CGTTTGATCCGTTCCATTCATTCAGGCTGTGTGCTACCCCGCTCAGAGTTGCCAGAAAAATTCTG	817
QY	141	AspGluLeuGlnGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyTyrPala	160
Db	818	GACGAGTTGCAGACCAATCGCTCGCTTATGTGTTTCCCTGTGCGTTGCTGGCTGGCGGCA	877
QY	161	MetMetGlyGlyAlaValAlaValLeuLeuGlyGlyGlyTyrGlnValSerIleuIleAla	180
Db	878	ATGATGAGGTGGCGCTGTGCTGTGCTGTGGGTGGGTGAGGAGGAGGTTTCCATAATTGCT	937
QY	181	PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyLysLysGlyLeuPro	200

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Db      938 TTTATACCGCGTTCACGATCATTCGCCAGCAGTATTTTGGGAAACAGGGTTGCT
Qy      201 ThrPhepGlnAsnValValGlyGlyPheIleAlaThrLeuProAlaSerIleAlaIleYr
Db      998 ACTTCTTCCAAATGTTGTGGTGTATTATGTCACGCGCTGCATCATTCCTTAT
Qy      221 SerLeuAlaLeuGlnPheGlyLeuGlnIleLysProSerGlnIleIleAlaSerGlyIle
Db      1058 TCTTGGCGGTGCAATTTGTTGATGATCAACCGCAGCCAGATCATCGCATCGAATT
Qy      241 ValValIleuLeuAlaGlyLeuThrLeuValGlnIleSerLeuGlnAsnGlyIleIleThrGlyAla
Db      1118 GTTGTGCTGTGGCAGGTTTACACTTGTGCAATCTTGCAGAGCAGCATACGCGGCGCT
Qy      261 ProValThrAlaSerAlaArgPhePheGlnThrLeuLeuPheThrGlyIleValAla
Db      1178 CCGGTGACAGCAGACGATGCGATTTTGAACACATCCCTGTTTACCGGCGGATGTTGCT
Qy      281 GlyValGlyLeuGlyIleGlnIleuSerGlnIleLeuHisValMetLeuProAlaMetGln
Db      1238 GGGGTGGGTTGGCGATTCAGCTTTCGAATCTTGATGATGATGCTGCGCATGAG
Qy      301 SerAlaAlaAlaProAsnIleSerSerThrPheAlaArgIleIleAlaGlyIleValThr
Db      1298 TCCGCTGACGACCTAATTTATTCGTCTACATTCGCCCGCATTTATCGCTGGTGGTACC
Qy      321 AlaAlaAlaPheAlaValGlyCysTyrAlaGlnIlePheSerValIleIleAlaGlyLeu
Db      1358 GCAGCGGCTTCGCGAGTGGGTGTTTACGCGGAGTGGTCTCGGATTTATTCGGGGCTT
Qy      341 ThrAlaIleuMetGlySerAlaPheTyrTyrLeuPheValValIleGlyIleProValSer
Db      1418 ACAGCGGTGATGGGTCTTGGGTTTATTACCTCTCTGTTTATTAGGCCCGCTCTCT
Qy      361 AlaAlaAlaIleAlaIleThrAlaValGlyPheThrGlyGlyLeuAlaAlaArgPhe
Db      1478 GCCGCTGCGATTTGCTGACAGAGGTTGGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCT
Qy      381 LeuIleProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla
Db      1538 TTGATTCACCGTTGATTTGGCGATGCGGATGATCAACCATGCTTCCAGGCTACGCA
Qy      401 IleTyrAlaGlyMetTyrAlaIleThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle
Db      1598 ATTTCGCGGGAATGAGCGCACCTTGAATGATCAACACTCATGGGTTTCCACCAACTT
Qy      421 AlaValAlaIleuAlaIleThrAlaSerSerIleuAlaAlaGlyValIleGlyIleTyrIle
Db      1658 GCGGTTGCTTTAGCCACTGCTTATCATCTTCCGCTGGCGTGGTTTGGGTGAGTGATT
Qy      441 AlaArgArgLeuArgArgProProArgPheAsnProTyrArgAlaPheThrIleAlaAsn
Db      1718 GCCCGCAGAGTACGTGCTCCACACGCTTCAACCCATACGTCATTTACCAAGGAGAT
Qy      461 GlnPheSerPheGlnIleGlnIleAlaGlnIleAsnGlnIleArgArgGlnIleArgProLys
Db      1778 GAGTTCTCTCCAGAGAGGCTGAGCAGAAATCAGCGCGGCAAGAAAAGCTCCAAAG
Qy      481 ThrAsnGlnArgPheGlyAsnLysArg 489
Db      1838 ACTAATCAAGATTCGTTAATATAAG 1864

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; TITLE OF INVENTION: L-THREONINE USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282413/MAS
; CURRENT APPLICATION NUMBER: US/09/963,521
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478.5
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: three-Gen
; US-09-963-521-1

Alignment Scores:
Pred. No.: 3,13e-263 Length: 2817
Score: 2432.00 Matches: 489
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-963-521-2 (1-489) x US-09-963-521-1 (1-2817)

Qy      1 MetLeuSerPheAlaThrLeuArgGlyArgIleSerThrValAspAlaIleAlaIleAla
Db      398 ATGTTGATTTTTCGACCCCTTCGTCGCGCATTTCAACATTCGTCGCAAAAGCCGCA
Qy      21 ProProProSerProIleuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal
Db      458 CCTCCCGCATCGCCACTAGCCCGCATGATCTCACTGACCATAGTCAAGTGGCGGCTGTG
Qy      41 MetAsnLeuAlaIleAlaIleGlyAspIleLeuLeuSerGlyThrSerAsnSerAsp
Db      518 ATGAAATTTGGCTCGAGAAATGGCGAATTTGCGAATTTCTTCTTCAAGTACGTAACAGTAT
Qy      458 ATGAAATTTGGCTCGAGAAATGGCGAATTTGCGAATTTCTTCTTCAAGTACGTAACAGTAT
Db      61 ThrIleValGlnAlaIleAlaIleAlaIleThrSerAlaTyrGlyLeuTyrThrHisValAsp
Qy      578 ACCAAGTGAAGTATGAGGAGTGAACCTCGCTATGCGCTGATACATAGCATGTGAT
Db      81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGlnArgLysMetProVal
Qy      638 ATCAGCTGAAATACGATACACATCTTCAACCAATCATGCTGATGAGAGGATGCCGCTC
Db      101 AsnValPheHisValValGlyLysLeuAspThrAsnPheSerIleuSerGlyValAsp
Qy      698 AACGTTTTCATGTTTGTGGCAGAGTTGACACCAACTTCTCCAAACGTCTGTGAGTTGAC
Db      121 ArgLeuIleArgSerIleGlnAlaGlyAlaIleThrProGlnIleValAlaGlyIleLeu
Qy      758 CGTTTATCCGTTCCATTCAGCTGTGCTACCCCGCTGAGGTTCCCGAAGAAATTTCTG
Db      141 AspGlnLeuGlnIleSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyTyrPala
Qy      818 GACGAGTTGAGCAACATCGCTGCTGATGTTTCCGTTGCTGCTGCTGCTGCTGCTGCTGCTG
Db      161 MetMetGlyGlyAlaValAlaValIleuLeuGlyGlyTyrGlnValSerLeuIleAla
Qy      878 ATGATGGGTGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
Db      181 PheIleThrAlaPheThrIleIleAlaIleThrThrSerPheLeuGlyLysLysGlyLeuPro
Qy      938 TTTATTTACCGCGTTCACGATCATTCGACAGCAGTCAATTTTGGGAAAGAGGTTTGCTT
Db      201 ThrPhepGlnAsnValValGlyGlyPheIleAlaIleThrLeuProAlaSerIleAlaIleYr
Qy      998 ACTTCTTCCAAATGTTGTGGTGTATTATGTCACGCGCTGCATCATTCCTTAT

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OY 221 SerLeuAlaLeuGlnPheGlyLeuGluLeuProSerGlnIleIleAlaSerGlyIle 240
DB 1058 TCTTTGGCGCTTGGATTGGTCTTGGATGACCAACCGGACGATCATCGATCGGAAAT 1117
OY 241 ValValIleuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyVala 260
DB 1118 GTTGTGCTGTTGGAGGTTTGACACTTGTCMACTCTGACGAGGCGGACATCACG9GCGCT 1177
OY 261 ProValThrAlaSerAlaArgPheGlyThrLeuLeuPheThrGlyGlyIleValAla 280
DB 1178 CCGGTGACAGCAATGACCACTTTTGAACAACCTCTGTTACGGCGGATTTGCT 1237
OY 281 GlyValGlyLeuGlyIleGlnLeuSerGlnIleLeuIleValMetLeuProAlaMetGlu 300
DB 1238 GGGGTGGGTTTGGGCACTTACGCTTTCGAAATCTTGACATGTCATGTCCTCGCATGAG 1297
OY 301 SerAlaAlaAlaProAsnTyrSerSerThrPheAlaArgIleIleAlaGlyValThr 320
DB 1298 TCCCTCGACGACCTAATTTATTTGTCATTCGCGCATTCGCGCATTCGCTGAGCGTACC 1357
OY 321 AlaAlaAlaPheAlaValGlyCysTyrAlaGluTyrPheSerValIleIleAlaGlyLeu 340
DB 1358 GCAGCGGCTTGGAGTGGTGTTCACCGGAGTGTCTCGGATTAATTCGCGGCTT 1417
OY 341 ThrAlaLeuMetGlySerAlaPheTyrTyrLeuPheValIleTyrLeuGlyProValSer 360
DB 1418 ACTCGCTGATGGGTTCTGCGTTTATTAACCTCTTCGTTTATTAAGGCGCGCTCT 1477
OY 361 AlaAlaAlaIleAlaIleThrAlaValGlyPheThrGlyIleLeuAlaAlaArgPhe 380
DB 1478 GCCCTGGATGTGTGCAACAGAGTGGTTTCATGAGTGGTGTGCTTGGCGCGTAC 1537
OY 381 LeuIleProPheLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400
DB 1538 TTGATTCACCGCTTATGTTGGCGATTCGCGGACATCACCAATCTTCCAGGTCTACA 1597
OY 401 IleTyrArgGlyMetTyrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle 420
DB 1598 ATTATACCGGAGATGTACGCCACCTTGATGATGATCAACCATCGGTTTCAACCAACT 1657
OY 421 AlaValAlaLeuAlaIleThrAlaSerSerLeuAlaAlaGlyValIleGlyValTyrPhe 440
DB 1658 GCGGTGCTTTAGCCACGCTTCATCATCTGCGCTGGCGTGGTGGTGGTGGTGGTGGT 1717
OY 441 AlaArgTyrLeuArgArgProProArgPheAsnProTyrArgAlaPheThrIleAsn 460
DB 1718 GCCGCGACGCTACGTCGTCACCAACGCTTCAACCCATACCGTGCATTTACCAAGCGCAT 1777
OY 461 GlnPheSerPheGlnGlnGlnAlaGlnGlnAsnGlnAlaGlnArgIleArgPheProIys 480
DB 1778 GAGTCTCTCTTCACAGAGAGAACTGACGCAATTCAGCGCGGACAGAAAGGTCGCAAG 1837
OY 481 ThrAsnGlnArgPheGlyAsnIleArg 489
DB 1838 ACTAATCAAGATTCGGTATATTAAGG 1864

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; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: ATCC14752
; NAME/KEY: CDS
; LOCATION: (398) ..(1864)
; OTHER INFORMATION: thrS gene
; US-09-834-721-1

Alignment Scores:
Pred. No.: 3,13e-263 Length: 2817
Score: 2432.00 Matches: 489
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-963-521-2 (1-489) x US-09-834-721-1 (1-2817)

OY 1 MetLeuSerPheAlaThrLeuArgGlyArgIleSerThrValAspAlaValAla 20
DB 398 ATGTTGAGTTTGGACCTTCGTCGCGCATTTCAACAGTTGACGCTGCAAAAGCGCA 457
OY 21 ProProSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal 40
DB 458 CCTCCGCCATCGCCACATGAGCCCGCATGATGATCTACACATAGTCAAGTGGCGGTGTG 517
OY 41 MetAsnLeuAlaAlaArgGlyIleValIleLeuLeuSerSerGlyThrSerAsnSerAsp 60
DB 518 ATGAAATTTGGCTGGACAGATATGGACATATTTGCTTCTTCAGGTACGTCMAACAGTAT 577
OY 61 ThrIleValGlnValAlaGlnAlaValThrSerAlaTyrGlyLeuTyrTyrThrIleValAsp 80
DB 578 ACCAAGGTGCAAGTTGACGCGGTACCTTCGATGAGCGTGTACTATACCATGTGAT 637
OY 81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGluArgIleMetProVal 100
DB 638 ATCAGTTGATATGATCATCATCATCATCTTCCAAACATCGGTGTGAGAGATGCGGCTC 697
OY 101 AsnValPheHisValValGlyIleValLeuAspThrAsnPheSerIleLeuValAsp 120
DB 698 AACGTTGATCATGTTGTGGGCAAGTTGGACACCAACTTCTCCAACTGTGAGGTATAC 757
OY 121 ArgLeuIleArgSerIleGlnAlaGlyAlaThrProProGluValAlaGluIleLeu 140
DB 758 CGTTTGATCCGTTCCATTCAGGCTGTGTCTACCCCGCTGAGGTTGCCGAGAAATTCG 817
OY 141 AspGluLeuGlnGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyTyrPhe 160
DB 818 GACGAGTTGACACATTCGCTCCGCTTATGTTTCCGTTGCGGTGGTGGTGGTGGTGGT 877
OY 161 MetMetGlyGlyAlaValAlaValLeuLeuGlyGlyIleTyrGlnValSerLeuIleAla 180
DB 878 ATGATGAGTGGGCGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 937
OY 181 PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyIleValIleLeuPro 200
DB 938 TTATATTCGCGCTTACATCATCTTCCACGACGTCATTTTGGAGAAAGAGGTTTGCT 997
OY 201 ThrPhePheGlnAsnValAlaGlyIlePheIleAlaThrLeuProAlaSerIleAlaTyr 220
DB 998 ACTTCTTCCAAAGATGTTGTGTGTATTTATGACAGCTGCTGCAATCGATGCTTAT 1057
OY 221 SerLeuAlaLeuGlnPheGlyLeuGluIleProSerGlnIleIleAlaSerGlyIle 240
DB 1058 TCTTTGGCGCTTGGATTGGTCTTGGATGACCAACCGGACGATCATCGATCGGAAAT 1117
OY 241 ValValIleuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyVala 260
DB 1118 GTTGTGCTGTTGGAGGTTTGACACTTGTCMACTCTGACGAGGCGGACATCACG9GCGCT 1177

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QY 261 ProValThrAlaSerAlaArgPhePheGluThrLeuLeuPheThrGlyGlyIleValAla 280
Db 1178 CCGGGAACAGACAGTGCACGATTTTTCAGAAACATCCGTTTACCGGGGACATGTTCT 1237
QY 281 GlyValGlyLeuGlyIleGlnLeuSerGluIleLeuHisValMetLeuProAlaMetGlu 300
Db 1238 GCGGCGGTTGGGCAATTCAGCTTCTGAAATCTTGCAATGTCATGTCCTCCGCGCATGGAG 1297
QY 301 SerAlaAlaAlaProAsnTyrSerSerThrPheAlaArgIleIleAlaGlyValThr 320
Db 1298 TCCCGTCGACGACCTTAATTTATTCCTCATTCGCCCGCATTCATTCGCTGGGGGTACCC 1357
QY 321 AlaAlaAlaPheAlaValGlyCysTyrAlaGluTyrPheSerSerValIleIleAlaGlyLeu 340
Db 1358 GCAAGCGCTTCGCAAGTGGGTTGTTCAGCGGAGTGGTCTCGATTAATTCGCGGCTT 1417
QY 341 ThrAlaLeuMetGlySerAlaPheTyrTyrLeuPheValIleTyrLeuGlyProValSer 360
Db 1418 ACTCGCTGATGGGTTCTGGCTTTATTAATCTCTTCCTGTTTATTAGCCCGCTCTCT 1477
QY 361 AlaAlaAlaIleAlaAlaThrAlaValGlyPheThrGlyGlyLeuAlaArgArgPhe 380
Db 1478 GCGCGTCGATGCTGCACAGCAGCAGTTGGTTTCACTGGTGGTGGTTCGCTGCATTC 1537
QY 381 LeuIleProProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400
Db 1538 TTGATTCACCGCTTGAATTTGGCGATTCGCGGACATCACCCAAATGCTTCACAGGCTTGC 1597
QY 401 IleTyrArgGlyMetTyrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle 420
Db 1598 ATTATACCGCGAAATGTACGACCTTGAATGATTAACAATCACTATGCTTCACCAATTT 1657
QY 421 AlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValLeuGlyGluTyrPhe 440
Db 1658 GCGGTTGCTTTAGCCATCGCTTCATCACTTGCCTGCGCGGTGGTGGTGGTGGTGGT 1717
QY 441 AlaArgArgLeuArgArgProProArgPheAsnProTyrArgAlaPheThrIleAlaAsn 460
Db 1718 GCCCGACAGGCTACGCTCCACACCGCTTACCCCAATACGTCATTTACCAAGGCGCAAT 1777
QY 461 GluPheSerPheGlnGlnGluAlaGluGlnAsnGlnArgArgGlnArgGlyAsnProGly 480
Db 1778 GAGTTCTCTCTTCACAGAGGAGAGCTGAGCAAAATCAGCGCGGAGAGAAAACGTTCCAAAG 1837
QY 481 ThrAsnGlnArgPheGlyAsnIleArg 489
Db 1838 ACTAATCAAGATTCGCTAATAAAAGG 1864

RESULT 13
US-09-783-388-1
; Sequence 1, Application US/09783388
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Petra
; APPLICANT: Eggeling, Lothar
; APPLICANT: Sahn, Hermann
; APPLICANT: Thiebach, Georg
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
; TITLE OF INVENTION: ENZYMATIC PRODUCTION OF L-THREONINE USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/277066
; CURRENT APPLICATION NUMBER: US/09/783,388
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum ATCC14752
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
US-09-783-388-1
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Alignment Scores:
Pred. No.: 3,13e-263 Length: 2817
Score: 2432.00 Matches: 489
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-963-521-2 (1-489) x US-09-783-388-1 (1-2817)

QY 1 MetLeuSerPheAlaThrLeuArgGlyArgIleSerThrValAspAlaAlaIleValAla 20
Db 398 ATGTTGATTTGGGACCCCTTCGTGGCGCATTCACAGTTGACGCTGCAAAAGCCCA 457
QY 21 ProProProSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal 40
Db 458 CTTCCGCGCATCGCACACAGCCCGCATTCATCTCACTGACCAATGATCAAGTGGCGGTGTG 517
QY 41 MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp 60
Db 518 ATGATTTGGCTGGAGAAATTTGGCGATTTTGTCTTCTCAAGGTACGTCAAAACAGTAT 577
QY 61 ThrIleValGlnValArgAlaValThrSerAlaTyrGlyLeuTyrTyrThrHisValAsp 80
Db 578 ACCAAGGTGCAAGTTGAGCGGTGACCTGCGTATGGCTGTACTATACCATGTGGAT 637
QY 81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGluArgGlyMetProVal 100
Db 638 ATACGTTGAATAGCATGCACCATCTTCACCAACATCGGTGTGGAGAGAAATGCCGCT 697
QY 101 AsnValPheHisValValGlyIleLeuAspThrAsnPheSerIleLeuSerGluValAsp 120
Db 698 AACGTTTATATTTGTTGGCAAGTTGGACACCAACTTCTCCAAAGTCTGAGGTTGAC 757
QY 121 ArgLeuIleArgSerIleGlnAlaGlyAlaThrProProGluValAlaGluIleLeu 140
Db 758 CGTTGATCCGTTCCATTCATGAGCTGAGTACCCTGCTAGGTTGCCGAAATTTCTG 817
QY 141 AspGluLeuGlnGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyTyrPhe 160
Db 818 GACGAGTTGGAGAAATCGCTGCTGTATGTTGCTTCCCTGTTGCTGTTGCTGGGCA 877
QY 161 MetMetGlyValAlaValAlaValLeuLeuGlyGlyIleThrGlnValSerLeuIleAla 180
Db 878 ATATGGGTGGCGCTGTGCTGCTGTTGGTGGTGAATGGAGGTTTCCCTTAATTTGCT 937
QY 181 PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyIleIleGlyLeuPro 200
Db 938 TTATATACCGGCTTCACGATCATTCACAGACGTATTTTGGGAAAGAGAGGTTTGCT 997
QY 201 ThrPhePheGlnAsnValValGlyIlePheIleAlaThrLeuProAlaSerIleAlaTyr 220
Db 998 ACTTCTTCAAAATGTTGTGGTGTATATGTCACACCTGCTGCATCGATTCCTAT 1057
QY 221 SerLeuAlaLeuGlnPheGlyLeuGluIleIleProSerGlnIleIleIleAsnSerGlyIle 240
Db 1058 TCTTTGGCTTGCATTTGTTGCTTTCATGATCAACAGCAGATTCATTCATTCGATTAAT 1117
QY 241 ValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyAla 260
Db 1118 GTTGGCTGTGGCAGGTTTGACATTCGATCTTCACAGAGCGGATCCAGGCGCT 1177
QY 261 ProValThrAlaSerAlaArgPhePheGluThrLeuLeuPheThrGlyGlyIleValAla 280
Db 1178 CCGGTGACAGCAAGTGCAGATTTTTCAGAAACATCCCTGTTTACCGGCGGCAATTTGCT 1237
QY 281 GlyValGlyLeuGlyIleGlnLeuSerGluIleLeuHisValMetLeuProAlaMetGlu 300
Db 1238 GCGGTGGGTTGGGCAATTCAGCTTCTGAAATCTTGCAATGTCATGTCCTCCGCGCATGGAG 1297
QY 301 SerAlaAlaAlaProAsnTyrSerSerThrPheAlaArgIleIleAlaGlyValThr 320
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Db 1298 TCCGCTGCAGACCTAATTAATTCGTCTACATTCGCCCGCATTAATCCGTGTGCGCTACCC 1357  
 QY 321 AAlaAlaAlaPheAlaValAlaGlyCysTyrAlaGluTrpSerValIleIleAlaGlyLeu 340  
 Db 1358 GAGAGCGGCTTCCGACGAGGTTGTACGCGAGTGGTCCCTCGGTATTAATTCGGGGCTT 1417  
 QY 341 ThrAlaLeuMetGlySerAlaPheTyrTyrLeuPheValValTyrLeuGlyProValSer 360  
 Db 1418 ACTGCGCTGATGGTCTCGCTTATTAATTCCTTCCTTGTATTAATTAAGGCCCGCTCTCT 1477  
 QY 361 AAlaAlaAlaIleAlaAlaThrAlaValAlaGlyPheThrGlyGlyLeuLeuAlaArgPhe 380  
 Db 1478 GCGGCTGCGATGTGTGACAGAGAGTTGTTCACTGTGTGTTCCTTGTGCGCGCATTC 1537  
 QY 381 IleuIleProPheLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400  
 Db 1538 TTGATTCACCGTTGATGTGGGATTCGCCGAGTACACCAATGCTTCACAGGCTCTACGA 1597  
 QY 401 IleTyrArgIleMetTyrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle 420  
 Db 1598 ATTACCGCGGAATGTAGCGCACCTTGAATGATCAACACATCATGGGTTTCACCAACATTT 1657  
 QY 421 AlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValValLeuGlyGluTrpIle 440  
 Db 1658 GCGGTCTCTTAGCCACGCTTCACTACCTGCGCTGCGGTTTTCGGTGAATGATTT 1717  
 QY 441 AlaArgIleuArgArgProProArgPheAsnProTyrArgAlaPheThrIleAsn 460  
 Db 1718 GCCCGAGGCTACGTCCTCCACCAAGCTTCAACCATACGTTGATTAACCAAGCCAAAT 1777  
 QY 461 GluPheSerPheGlnGluGluAlaGluGlnAsnGlnArgGlnArgGlyValArgProLys 480  
 Db 1778 GAGTTCCTCTCCAGGAGGAGCTGAGCAATCAGCGCGCGAGAAACGTCCAAAG 1837  
 QY 481 ThrAsnGlnArgPheGlnAsnLysArg 489  
 Db 1838 ACTAATCAAGATTGCGTAATTAAGG 1864

## RESULT 14

US-09-951-535-1

; Sequence 1, Application US/09951535  
 ; Publication No. US20030049802A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ZIEGLER, PETRA  
 ; APPLICANT: SAHM, HERMANN  
 ; APPLICANT: EGGELING, LOTMAR  
 ; APPLICANT: THIERBACH, GREGG  
 ; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND  
 ; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE  
 ; FILE REFERENCE: 21123/282415/MAS  
 ; CURRENT APPLICATION NUMBER: US/09/951,535  
 ; CURRENT FILING DATE: 2001-09-14  
 ; PRIOR APPLICATION NUMBER: 09/431,099  
 ; PRIOR FILING DATE: 1998-11-01  
 ; PRIOR APPLICATION NUMBER: DE 199 41 478.5  
 ; PRIOR FILING DATE: 1999-09-01  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 2817  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium glutamicum  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (398)..(1864)  
 ; OTHER INFORMATION: thrB-Gen  
 ; US-09-951-535-1

## Alignment Scores:

Pred. No.: 3,13e-263 Length: 2817  
 Score: 2432.00 Matches: 489  
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0  
 US-09-963-521-2 (1-489) x US-09-951-535-1 (1-2817)  
 QY 1 MetLeuSerPheAlaThrLeuArgIleArgIleSerThrValAspAlaValAla 20  
 Db 398 ATGTTAGATTTCGACACCTCGTGGCCGCAATTCACAGTTGACGCTGCAAAAGCCGCA 457  
 QY 21 ProProProSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal 40  
 Db 458 CTTCCCGCATCGCCACATGAGCCCGATGATGATCACTACATAGTCAAGTGGCCGGGTG 517  
 QY 41 MetAsnLeuAlaIleArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp 60  
 Db 518 ATGAATTTGGCTCGAGAAATGGGATATTTTGTCTTCTTCAGGTACGTCAAAAGATGAT 577  
 QY 61 ThrIleValGlnValArgAlaValThrSerAlaTyrGlyLeuTyrThrHisValAsp 80  
 Db 578 ACCAAGTGCAGATTCAGAGCGGTGACCTCGGTATGCGCTGTACTATACGATGTGGAT 637  
 QY 81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGluArgLysMetProVal 100  
 Db 638 ATCAGCTTGAATACGATCACCATCTTCCACCAACATCGGTGAGAGAGAAATGCCGATC 697  
 QY 101 AsnValPheHisValValAlaGlyLysLeuAspThrAsnPheSerLysLeuSerGluValAsp 120  
 Db 698 AACGTGTTCAATGTTGGGCGCAATTTGACACCAACTTCTCCAAACTGTGAGGTTGAC 757  
 QY 121 ArgLeuIleArgSerIleGlnAlaGlyAlaThrProProGluValAlaGluLysIleLeu 140  
 Db 758 CGTTGATTCGCTTCATTCAGCTGAGTGTACCCGCTGAGGTTGCCGCAAAATTCGTG 817  
 QY 141 AspGluLeuGlnGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyTyrAla 160  
 Db 818 GACGAGTTGAGCAATGCGCTGCTTATGTTCTCTGTTGGTTCCTTGGCTGGCGCA 877  
 QY 161 MetMetGlyGlyValAlaValAlaLeuLeuGlyGlyTyrGlnValSerLeuIleAla 180  
 Db 878 ATGATGGGTGGCGCTGTTGCTGTGTGTGGTGTGGATGGCAGGTTTCCCTAATTCGT 937  
 QY 181 PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyLysGlyLeuPro 200  
 Db 938 TTATATTCGCGCTTCACGATCATTCGCCACGATCATTTTGGGAAAGAGGTTTGGCT 997  
 QY 201 ThrPhePheGlnAsnValAlaGlyGlyPheIleAlaThrLeuProAlaSerIleAlaTyr 220  
 Db 998 ACTTTCCTCCAAAATGTTGTTGGTGTATTTGTCACGCTGCTGCATTCGATTCCTTAT 1057  
 QY 221 SerLeuAlaLeuGlnPheGlyLeuGluIleLysProSerGlnIleIleAlaSerGlyIle 240  
 Db 1058 TCTTTGGCGTTGCAATTTGGTCTTGATCAACACGAGCAGATCATGCAATCGGAATT 1117  
 QY 241 ValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyAla 260  
 Db 1118 GTTGTGCTGTGGCAGGTTTGACCTTGCAATCTTCGACAGAGCGGATTCACG36CGT 1177  
 QY 261 ProValThrAlaSerAlaArgPhePheGlnThrLeuLeuPheThrGlyIleValAla 280  
 Db 1178 CCGGTGACAGCAAGTGCAGATTTTGTGAACACTCTGTTTACCGCGCGCATTTGTGCT 1237  
 QY 281 GlyValAlaGlyLeuGlyIleGlnLeuSerGluIleLeuHisValMetLeuProAlaMetGlu 300  
 Db 1238 GCGGTGGGTTTGGGATTCAGCTTCTGAATCTTGCAATGTCATGTGCTGCGCATGGAG 1297  
 QY 301 SerAlaAlaAlaProAsnTyrSerThrPheAlaArgIleIleAlaGlyGlyValThr 320  
 Db 1298 TCCGCTGCAGACCTAATTAATTCGTCTACATTCGCCCGCATTAATGCTGTGCGCTACCC 1357  
 QY 321 AAlaAlaAlaPheAlaValAlaGlyCysTyrAlaGluTrpSerSerValIleIleAlaGlyLeu 340  
 Db 1358 GAGAGCGGCTTCCGACGAGGTTGTACGCGAGTGGTCCCTCGGTATTAATTCGGGGCTT 1417



Db	1538	TTGATTCACCGCGTGAATGTGTGGCATGTCGGGACATCACCAACCAATGGCTCCAGGCTCTAGCA	1597
Oy	401	IIleYrYrgrgYmeYtYrAlaThrLeuAsnAspGlnThrLeuMetGlypHeThrAsnIle	420
Db	1598	ATTTCACGGCGGAATGTATACGCCACCTTGATATATCAACACTCACTACGGGTTTACCAACATT	1657
Oy	421	AlaValAlaIleuAlaThrAlaSerSerIleuAlaIaGlyValIleuGlyGluTrpIle	440
Db	1658	GCGGTTCGCTTAGCCACCTGCTTCATCACTTCGCCCTGGCGGTGGTGGTGGATGGAGT	1717
Oy	441	AlaArgArgLeuArgArgProProArgPheAsnProTYrArgAlaPheThrLysAlaAsn	460
Db	1718	GCCCGCGAGCTACGTCGTCCACCGCTTCAACCCATACCTGTGATTTACCAAGCGAAT	1777
Oy	461	GluPheSerPheGlnGluGluAlaGluGlnAsnGlnArgArgGlnArgLysArgProLys	480
Db	1778	GAGTTCCTCCTCCAGGAGGAAGCTGACGACGAATCAGCCGCGAGAGAAAACTGTCCAAG	1837
Oy	481	ThrAsnGlnArgPheGlyAsnLysArg	489
Db	1838	ACTATATCAAGATTTCGTATATTAAGG	1864

Search completed: July 31, 2004, 11:47:08  
Job time : 632 secs



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OM nucleic - nucleic search, using sw model

Run on: July 31, 2004, 00:43:11 ; Search time 134.915 Seconds  
(without alignments)  
7852.389 Million cell updates/sec

Title: US-09-963-521-3

Perfect score: 1909

Sequence: 1 agcttgcatcctcgcagtc.....aaaccgcagccggtacgc 1909

Scoring table: IDENTITY NUC

Searched: 682709 seqs, 277475446 residues 1365418

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:\*

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6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1909	100.0	1909	4	US-09-431-099-3
2	1836.6	96.2	2817	4	US-09-431-099-1
3	86.6	4.5	4403765	3	US-09-103-840A-2
4	86.6	4.5	4411529	3	US-09-103-840A-1
5	47.6	2.5	7218	1	US-08-232-463-14
6	46.6	2.4	400	4	US-08-956-171E-4234
7	45.8	2.4	1230025	4	US-09-198-452A-1
8	45.6	2.3	381	4	US-08-956-171E-4023
9	44.4	2.3	237	4	US-08-956-171E-4566
10	44.4	2.3	239	4	US-08-956-171E-4543
11	44.4	2.3	239	4	US-08-956-171E-4544
12	44.4	2.3	400	4	US-08-956-171E-3531
13	44.4	2.3	400	4	US-08-956-171E-3560
14	44.4	2.3	400	4	US-08-956-171E-4198
15	44.4	2.3	411	4	US-08-956-171E-4353
16	44.4	2.3	475	4	US-08-956-171E-3621
17	44.4	2.3	6591	4	US-08-956-171E-3114
18	43.4	2.3	400	4	US-08-956-171E-3542
19	43.4	2.3	400	4	US-08-956-171E-3723
20	43.4	2.3	1171	4	US-08-956-171E-3539
21	42	2.2	339	4	US-08-956-171E-4663
22	41.2	2.2	400	4	US-08-956-171E-4029
23	40	2.1	2870	5	PCT-US93-07213-3
24	39.8	2.1	713	2	US-08-706-702-26
25	39.8	2.1	713	3	US-08-706-706-26
26	39.8	2.1	713	4	US-09-238-471-26
27	39.8	2.1	1308	4	US-09-577-424-4

28	39.8	2.1	12614	4	US-09-577-424-1	Sequence 1, Appli
C 29	39.2	2.1	399	4	US-09-621-976-8976	Sequence 8976, Ap
C 30	39.2	2.1	1232	2	US-08-189-256A-8	Sequence 8, Appli
C 31	39.2	2.1	1232	4	US-09-193-853-8	Sequence 8, Appli
C 32	39	2.0	72	2	US-08-585-585A-11	Sequence 11, Appli
C 33	39	2.0	81	3	US-08-685-808-10	Sequence 10, Appli
C 34	39	2.0	3681	1	US-08-505-860C-10	Sequence 10, Appli
C 35	39	2.0	4539	1	US-08-924-028A-6	Sequence 6, Appli
C 36	39	2.0	4539	1	US-08-119-512-1	Sequence 1, Appli
C 37	39	2.0	4539	1	US-08-488-015B-1	Sequence 1, Appli
C 38	39	2.0	4542	3	US-08-814-412-11	Sequence 11, Appli
C 39	39	2.0	5314	1	US-07-924-028A-4	Sequence 4, Appli
40	38.8	2.0	59	4	US-08-956-171E-4959	Sequence 4959, Ap
41	38.6	2.0	586	1	US-08-046-583-10	Sequence 10, Appli
42	38.6	2.0	586	1	US-08-956-171E-4198	Sequence 1, Appli
43	38.6	2.0	586	2	US-08-331-355A-22	Sequence 22, Appli
44	38.6	2.0	586	5	PCT-US94-12364-22	Sequence 22, Appli
45	38.6	2.0	586	5	PCT-US95-07753-1	Sequence 1, Appli

## ALIGNMENTS

RESULT 1

US-09-431-099-3

Sequence 3, Application US/09431099

Patent No. 6410705

GENERAL INFORMATION:

APPLICANT: Degussa-Höls AG

APPLICANT: Forschungszentrum-Joachim GmbH

TITLE OF INVENTION: New nucleotide sequences coding for the thr3 gene and process for

FILE REFERENCE: 990079 BT

CURRENT FILING DATE: 1999-11-01

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 1909

TYPE: DNA

ORGANISM: Corynebacterium glutamicum ATCC13032

FEATURE:

NAME/KEY: CDS

LOCATION: (280)..(1746)

OTHER INFORMATION: thr3-Gen

US-09-431-099-3

Query Match

Best Local Similarity 100.0%; Score 1909; DB 4; Length 1909;

Matches 1909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AGTTGCATGCGCGAGTGTGATCTTAAGAGATCCCGCCCTTGAAGCTGCTGTTATGA	60
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QY	61	GCTGAGAGAGACTTGAATCTCAACTACGATTAAGAGTGTGCGTCCGATTTG	120
DB	61	GCTGAGAGAGACTTGAATCTCAACTACGATTAAGAGTGTGCGTCCGATTTG	120
QY	121	CGGCACTCCAGACCGGAGATGCTGATGATCAAGAACTAGAAATGATCTTACGAT	180
DB	121	CGGCACTCCAGACCGGAGATGCTGATGATCAAGAACTAGAAATGATCTTACGAT	180
QY	181	GCTGATCAATGAGATGCGGCTAGATCTGATGAGACCGTGCATTAACGACCTG	240
DB	181	GCTGATCAATGAGATGCGGCTAGATCTGATGAGACCGTGCATTAACGACCTG	240
QY	241	TAATGAGATCTTCTTCTTCTTCAAAATGTTTCCAGCGGATGTTGACCTT	300
DB	241	TAATGAGATCTTCTTCTTCTTCAAAATGTTTCCAGCGGATGTTGACCTT	300
QY	301	CGTGGCGGATTTCAACAGTTGACGCTGCAAAAGCGGACCTCCGATCGCCACTAGCC	360
DB	301	CGTGGCGGATTTCAACAGTTGACGCTGCAAAAGCGGACCTCCGATCGCCACTAGCC	360

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Db 301 CGTGGCCGATTTCAACAGTTGACGTGCAAAAGCCGCACTCCGCATGCGCATAGCC 360
OY 361 CCGATTGATCTCACTGACACATAGTCAAGTGGCCGGTGTGAATTTGGTCCGAGAATT 420
Db 361 CCGATTGATCTCACTGACACATAGTCAAGTGGCCGGTGTGAATTTGGTCCGAGAATT 420
OY 421 GGGCAATATTTGCTTTCTTCAAGTACGTCAAAATGTGACACCAAGTACAAAGTTCCAGCA 480
Db 421 GGGCAATATTTGCTTTCTTCAAGTACGTCAAAATGTGACACCAAGTACAAAGTTCCAGCA 480
OY 481 GTGACCTGTGGTGAAGTTGTATCAACGACCGGTGATCACTGTAATATCATGATCACC 540
Db 481 GTGACCTGTGGTGAAGTTGTATCAACGACCGGTGATCACTGTAATATCATGATCACC 540
OY 541 ATCTTCAACCAATCGTGTGAGAGAGAAAGTCCGATCAAGTGTTCATGTTGAGGC 600
Db 541 ATCTTCAACCAATCGTGTGAGAGAGAAAGTCCGATCAAGTGTTCATGTTGAGGC 600
OY 601 AAGTTGACACCAACTTCTCCAACTGTCTGAGTTGACCGTTGATCCGTTCAATTCAG 660
Db 601 AAGTTGACACCAACTTCTCCAACTGTCTGAGTTGACCGTTGATCCGTTCAATTCAG 660
OY 661 GCTGGTGGACCCCGCCTGAGTGGCCGAGAAAATCTGAGACGAGTTGAGCAATCCCT 720
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OY 721 GCGTCTTAATGTTTCCCTGTTGCGTTGCTGAGGCAATGATGGTGTGCTGTTGCT 780
Db 721 GCGTCTTAATGTTTCCCTGTTGCGTTGCTGAGGCAATGATGGTGTGCTGTTGCT 780
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Db 781 GTGCTGTTGGTGTGATGAGTGGCAAGTTCCCTAATGTTTATTAACCGGCTGACGATC 840
OY 841 ATTGCCACGACGTCAATTTTGAGAAAGAGTTTCCCTACTTTCTTCCAAATGTTGTT 900
Db 841 ATTGCCACGACGTCAATTTTGAGAAAGAGTTTCCCTACTTTCTTCCAAATGTTGTT 900
OY 901 GGTGGTTTATTTGCGACGCTGCTGATGATGCTTATTTGCTTGGCTTGGCAATTTGCT 960
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OY 1021 ACACCTGTCGATCTCTGACAGGACGAGATCACGAGCGCTCCGATGACAGCAAGTGCACGA 1080
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Db 1081 TTTTTCGAAAACATCTCTGTTTACCGGCGGCAATTTGCTGCGGTGGGTTTGGGCAATTCAG 1140
OY 1141 CTTTCGAAATCTGCAATGTCATGTTGCTGTCATGAGATCCGCTGACGACCACTTAATAT 1200
Db 1141 CTTTCGAAATCTGCAATGTCATGTTGCTGTCATGAGATCCGCTGACGACCACTTAATAT 1200
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Db 1201 TCGTCTACATTCGCGCGCATTAATGCTGTGAGCGTCAACGCGACGCGCTTCCAGTGGGT 1260
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Db 1321 TTTTATTAACCTGCTGTTTATTTAATGAGCCCGCTCTGCGGCTGCGATTCGCAACA 1380
OY 1381 GCAAGTTGGTTTCACTGAGTGTGCTTGGCCGTCGATTCGTAATTCACCGTTGATGTG 1440
Db 1381 GCAAGTTGGTTTCACTGAGTGTGCTTGGCCGTCGATTCGTAATTCACCGTTGATGTG 1440

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OY 1441 GCGATTCCCGGCAATTCACCAATGCTTCCAGGTCTAGCAATTTTACCGGGAATGTAGCC 1500
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OY 1501 ACCCTGAATGATCAAACTCATGAGTTTTCACCAATTCGAGTGTCTTAAAGCCACTGCT 1560
Db 1501 ACCCTGAATGATCAAACTCATGAGTTTTCACCAATTCGAGTGTCTTAAAGCCACTGCT 1560
OY 1561 TCATCACTTCCGCTGCGCTGTTTGGTGTGATGATGATGCGCCAGGCTAACGTGCTCA 1620
Db 1561 TCATCACTTCCGCTGCGCTGTTTGGTGTGATGATGATGCGCCAGGCTAACGTGCTCA 1620
OY 1621 CCAGCTTCAACCCATTCGCGGATTTTACCAAGGCGAATGATGCTCTTCCAGAGAGAA 1680
Db 1621 CCAGCTTCAACCCATTCGCGGATTTTACCAAGGCGAATGATGCTCTTCCAGAGAGAA 1680
OY 1681 GCTGAGCAGATCAGCCCGCAGAGAAAACGTCCAAAGACTAATCAGAGATTGCTAAT 1740
Db 1681 GCTGAGCAGATCAGCCCGCAGAGAAAACGTCCAAAGACTAATCAGAGATTGCTAAT 1740
OY 1741 AAAAGTAAAAATCAACTGCTTAGGGCTTTTGGCTTAAATAGCTGATATCGGGTTC 1800
Db 1741 AAAAGTAAAAATCAACTGCTTAGGGCTTTTGGCTTAAATAGCTGATATCGGGTTC 1800
OY 1801 GATGCTTTTAAACATCAGAGAGATCCTTSCCGGCAAAATCAGACACTGCTCCAC 1860
Db 1801 GATGCTTTTAAACATCAGAGAGATCCTTSCCGGCAAAATCAGACACTGCTCCAC 1860
OY 1861 CCAGAAATCCCTTCACTGCTGTGTAAGAGAAAACCGACCGCGGGTACCG 1909
Db 1861 CCAGAAATCCCTTCACTGCTGTGTAAGAGAAAACCGACCGCGGGTACCG 1909

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RESULT 2
US-09-431-099-1
; Sequence 1, Application US/09431099
; Patent No. 6410705
; GENERAL INFORMATION:
; APPLICANT: Degussa-Höls AG
; APPLICANT: Forschungszentrum-Jülich GmbH
; TITLE OF INVENTION: New nucleotide sequences coding for the thr gene and process for
; FILE REFERENCE: 990079 BT
; CURRENT APPLICATION NUMBER: US/09/431,099
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum ATCC14752
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: thrf-gen
US-09-431-099-1

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Query Match 96.2%; Score 1836.6; DB 4; Length 2817;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1848; Conservative 19; Indels 0; Gaps 0;
OY 38 CCCCTTGAACCTGCTGTTATTTAGCTGAGAGAGACTTGAACCTCAACCTTACGCAATTA 97
Db 156 CCCCTTGAACCTGCTGTTATTTAGCTGAGAGAGACTTGAACCTCAACCTTACGCAATTA 215
OY 98 CAAGTGGTGGTGGTCCCAATTTGCGCACTCCAGACCGGAGATGCTGATCAACAAC 157
Db 216 CAAGTGGTGGTGGTCCCAATTTGCGCACTCCAGACCGGAGATGCTGATCAACAAC 275
OY 158 TAGCAATAGTATCTTAGGCTATGCTGATACATCAATGAAATTCGGGGCTAGAGTATCTG 217
Db 276 TAGCAATAGTATCTTAGGCTATGCTGATACATCAATGAAATTCGGGGCTAGAGTATCTG 335

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QY 218 GTGAACCGTGATGAAAGCACTGTGATGAACTCTTTTCTTCCAAATGTTTTCAGC 277  
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 Db 396 GGATGTTGATGTTTGGCGACCTTGGTGGCGGCAATTTTCAACAGTTGAGCTTCCAAACCG 455  
 QY 338 CACCTCCGCAATGCACTAGCCCCGATGATCTCAGTACCATAGTCAAGTGGCCGATG 397  
 Db 456 CACCTCCGCAATGCACTAGCCCCGATGATCTCAGTACCATAGTCAAGTGGCCGATG 515  
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 Db 516 TGATGAATTTGGCTGCGAAGATTGGCGAATTTTGGCTTTCTTCAGGTAAGTCAATAAGT 575  
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 QY 518 ATATCAAGTTGAATACGATCAACATCTTCAACCAATGAGTGGAGAGAGAGATGCGCG 577  
 Db 636 ATATCAAGTTGAATACGATCAACATCTTCAACCAATGAGTGGAGAGAGAGATGCGCG 695  
 QY 578 TCAACGTTTTCATGTTGAGGCAAGTTGGAACCAACTTCTCCAACTGTCTGAGGTTG 637  
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 QY 638 ACCGTTGATCCGTTGCACTCAGGCTGGTGGAGCAACCCGCGCTGAGTGGCCGAGAAATCC 697  
 Db 756 ACCGTTGATCCGTTGCACTCAGGCTGGTGGAGCAACCCGCGCTGAGTGGCCGAGAAATCC 815  
 QY 698 TGAACGATGAGCAATCCCTGCGCTCTATGAGTTTCCCTGTTGCGTTGCGTGGG 757  
 Db 816 TGAACGATGAGCAATCCCTGCGCTCTATGAGTTTCCCTGTTGCGTTGCGTGGG 875  
 QY 758 CAATGATGGTGTGCTGTGCTGTGCTGTGTTGGTGGTGGATGGCAGGTTTCCCTAATTG 817  
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 QY 818 CTTTATTTACCGGTTGAGCATTTGCGCAAGCAAGTCAATTTTGGGAAAGAGGTTTGC 877  
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 QY 1058 CTCGCGTGAACGCAAGTGAACATTTTTCGAAAACCTCTGTTTACCGGCGGATTTGTT 1117  
 Db 1176 CTCGCGTGAACGCAAGTGAACATTTTTCGAAAACCTCTGTTTACCGGCGGATTTGTT 1235  
 QY 1118 CTGGCGTGGGTTTGGGCAATTCAGCTTTTGAATCTTTCGATGTCATGTTGCTGCGCATGG 1177  
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 QY 1178 AGTCGCTGAGCAACCAATTTATTCGTTCAATTCGCGCGCATTAATGCGTGGGCGTCA 1237  
 Db 1296 AGTCGCTGAGCAACCAATTTATTCGTTCAATTCGCGCGCATTAATGCGTGGGCGTCA 1355  
 QY 1238 CCGCAGCGGCTTTCGAGTGGGTTGTTACGCGGAGTGGTCTCGATTAATTCGCGGCG 1297  
 Db 1356 CCGCAGCGGCTTTCGAGTGGGTTGTTACGCGGAGTGGTCTCGATTAATTCGCGGCG 1415

QY 1298 TTAAGCGGTGATGAGGTTTGGCTGTTTATTAACCTCTTGGTGTATTTAGAGCCCGCT 1357  
 Db 1416 TTAAGCGGTGATGAGGTTTGGCTGTTTATTAACCTCTTGGTGTATTTAGAGCCCGCT 1475  
 QY 1358 CTGCGCGTGGGATTTGCTGCAACAGAGTGGTTTCACTGTTGTTGCTTGGCGTGGAT 1417  
 Db 1476 CTGCGCGTGGGATTTGCTGCAACAGAGTGGTTTCACTGTTGTTGCTTGGCGTGGAT 1535  
 QY 1418 TCTGATTTCCACGCTGATTTGGCGGATTTGCGGCACTCACACCAATGCTTCAGTGTAG 1477  
 Db 1536 TCTGATTTCCACGCTGATTTGGCGGATTTGCGGCACTCACACCAATGCTTCAGTGTAG 1595  
 QY 1478 CAATTTACCGCGGATGTAAGCCCACTGATGATCAACCAATGATGATGATGATGATGATG 1537  
 Db 1596 CAATTTACCGCGGATGTAAGCCCACTGATGATCAACCAATGATGATGATGATGATGATG 1655  
 QY 1538 TTGGGTTGCTTTTACGCACTGCTTCACTGCTGGCGCTGGGCTGTTTGGGTTGAGTGA 1597  
 Db 1656 TTGGGTTGCTTTTACGCACTGCTTCACTGCTGGCGCTGGGCTGTTTGGGTTGAGTGA 1715  
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 Db 1896 TAAATAGCGTGAATATTCGGGTGATGCTGTTTAAACATCTCAGAGAGATCCTTGGCGGCG 1955  
 QY 1838 AAAATCAAGCACTGCTCCACCCCAAGATCCCTTCAAGCTGTTGAAGAGAAACCGCA 1897  
 Db 1956 AAAATCAAGCACTGCTCCACCCCAAGATCCCTTCAAGCTGTTGAAGAGAAACCGCA 2015  
 QY 1898 GCCGGGG 1904  
 Db 2016 GCCGGTG 2022

RESULT 3  
 US-09-103-840A-2  
 ; Sequence 2, Application US/09103840A  
 ; Patent No. 6294328  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FLEISCHMAN, Robert D.  
 ; APPLICANT: WHITE, Owen R.  
 ; APPLICANT: PRASER, Claire M.  
 ; APPLICANT: VENTER, John C.  
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
 ; FILE REFERENCE: 24366-20007.00  
 ; CURRENT APPLICATION NUMBER: US/09/103,840A  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 4403765  
 ; TYPE: DNA  
 ; ORGANISM: Mycobacterium tuberculosis  
 ; FEATURE:  
 ; OTHER INFORMATION: CDC 1551  
 ; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
 ; OTHER INFORMATION: represent a, t, c or g  
 US-09-103-840A-2  
 Query Match 4.5%; Score 86.6; DB 3; Length 4403765;  
 Best Local Similarity 45.6%; Pred. No. 3; 4e-15;

Matches	498;	Conservative	0;	Mismatches	559;	Indels	36;	Gaps	4;
QY	531	TACGATCACCATTCTTCAACACATCGGTGTGAGAGAGAAAGTCCGCTCAACGTTTCA	590						
Db	4180213	TACGATCACCATTCTTCAACACATCGGTGTGAGAGAGAAAGTCCGCTCAACGTTTCA	4180272						
QY	591	TGTTGTAGGAGATTTGACACCACTTCTCAAACTGTCTGAGGTGACCGTTGATCCG	650						
Db	4180273	GTGCGTCCGAGCCGCTGACATGACTAGACCGGCTGACCACTCGATGCACTGCTTCA	4180332						
QY	651	TTCCATTAGGCTGTGAGACCCGCTGAGAGTTGCCAGAAATCTCGACGAGTTGGA	710						
Db	4180333	GCGGATTAACCTCCGCTGCGCTGTGAGTGCACAGGCTCAGAGGCTATGACGAGTTAC	4180392						
QY	711	GCAATCCCTGCTGTTATGAGTTTCCCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG	770						
Db	4180393	CGAAGCGGCCACCCCTACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4180452						
QY	771	TGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	830						
Db	4180453	CGGCGTCCGACATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4180512						
QY	831	GTTACAGCATTTGACAGACGATCTTTTGGAAAGAGGATTTGCTTCTTCTTCA	890						
Db	4180513	TGGGCTGATTCACGACCTGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4180572						
QY	891	AAATGTTGTTGTTGTTTATTTTCCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	950						
Db	4180573	GCGGCTGTTGCGCGGAGATGCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4180632						
QY	951	GCAATTTGCTTGTAGATCAACAGGACATCATGCTGCTGCTGCTGCTGCTGCTGCTG	1010						
Db	4180633	CCA-----GATTCGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4180677						
QY	1011	GCGAGTTTGAACATCTGTCATCTCTGACAGACGACATCAACGCGCTGCTGCTGACG	1070						
Db	4180678	GTTCTGAGATGACTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4180737						
QY	1071	AAGTGCAGATTTTGTGAAACATCTCTGTTTACGCGCGCATTTGCTGCTGCTGCTG	1124						
Db	4180738	ACTGCGCGGCTGCTGCGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4180797						
QY	1125	-----GGTTTGGGCACTTACGCTTGTGAATCTTGTGATGATGCTGCTGCTGCTG	1175						
Db	4180798	CTGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4180857						
QY	1176	GGAATCCGCTGACGACCTAATTTATGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTG	1235						
Db	4180858	GACGCTGCCACCCGCGGCTATGCGCTATCGATCTGCTGCTGCTGCTGCTGCTGCTG	4180917						
QY	1236	CACGCGAGCGCTTGTGAGTGGTTTGAACGCGAGTGTCTGCTGCTGCTGCTGCTGCTG	1295						
Db	4180918	GTCCGCGCTGTGCTGACGATGCGAGCTATGCGCGCTGCTGCTGCTGCTGCTGCTG	4180977						
QY	1296	GCTTACTG-----GCTGATGAGTTTGTGCTTATTAACCTTGTGCTTATTAAGCC	1352						
Db	4180978	ACTCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4181037						
QY	1353	GCTCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1412						
Db	4181038	AGTGTGCGCACTGGAACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4181097						
QY	1413	TGCTATTTGATTTTCAACGCTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1472						
Db	4181098	CGGTGCGAGGCTTCCGCTTGTGATGACGCGCACCGCGGCTGCTGCTGCTGCTGCTG	4181157						
QY	1473	TCTAGCAATTTTACCGGGAATGTACG-----CACCTGATGATCAAAACATGAGGTTT	1529						
Db	4181158	CTTGTGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4181217						
QY	1530	CACCAACATTTGCGGTTGCTTTAGCACTGCTTCACTTGGCTGCTGCTGCTGCTGCTG	1589						
Db	4181218	GACCAAGCTGTGGAAGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4181277						

QY	1590	TGAGTGGATTGCC	1602						
Db	4181278	CGAGTTCTTCGCC	4181290						
<p>                     RESULT 4                      US-09-103-840A-1                      ; Sequence 1, Application US/09103840A                      ; Patent No. 6294528                      ; GENERAL INFORMATION:                      ; APPLICANT: FLEISCHMAN, Robert D.                      ; APPLICANT: WHITE, Owen R.                      ; APPLICANT: FRASER, Claire M.                      ; APPLICANT: VENTNER, John C.                      ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM                      ; TITLE OF INVENTION: TUBERCULOSIS                      ; FILE REFERENCE: 24366-20007.00                      ; CURRENT APPLICATION NUMBER: US/09/103.840A                      ; CURRENT FILING DATE: 1998-06-24                      ; NUMBER OF SEQ ID NOS: 2                      ; SOFTWARE: Patentin Ver. 2.1                      ; SEQ ID NO 1                      ; LENGTH: 4411529                      ; TYPE: DNA                      ; ORGANISM: Mycobacterium tuberculosis                      ; OTHER INFORMATION: H37Rv                      US-09-103-840A-1                 </p>									
<p>                     Query Match 4.5%; Score 86.6; DB 3; Length 4411529;                      Best Local Similarity 45.6%; Pred. No. 5.4e-15;                      Matches 498; Conservative 0; Mismatches 559; Indels 36; Gaps 4;                 </p>									
QY	531	TACGATCACCATTCTTCAACACATCGGTGTGAGAGAGAAAGTCCGCTCAACGTTTCA	590						
Db	4187965	TACGATCACCATTCTTCAACACATCGGTGTGAGAGAGAAAGTCCGCTCAACGTTTCA	4188024						
QY	591	TGTTGTAGGAGATTTGACACCACTTCTCCAACTGTCTGAGTTGACCGTTGATCCG	650						
Db	4188025	GTGCTGCGGACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4188084						
QY	651	TTCCATTAGGCTGTGAGACCCGCTGAGAGTTGCCAGAAATCTCGACGAGTTGGA	710						
Db	4188085	GCGGATACCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4188144						
QY	711	GCAATCCCTGCTGCTTATGTTTCCCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	770						
Db	4188145	CGAAGGCCCCCACTTACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4188204						
QY	771	TGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	830						
Db	4188205	CGGCTGCGCACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4188264						
QY	831	GTTACGATCAATGCGACGATCTTTTGGGAAAAGAGGTTTCCCTACTTTCTTCA	890						
Db	4188265	TGGCTGATTCACGCACTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4188324						
QY	891	AAATGTTGTTGTTTATTTTGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	950						
Db	4188325	GCGGCTGTTGCGCGGAGATGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4188384						
QY	951	GCAATTTGCTTGTGATCAACCGAGCCAGATCACTGCTGCTGCTGCTGCTGCTGCTG	1010						
Db	4188385	CCA-----GATTCGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4188429						
QY	1011	GCGAGTTTGAACATCTGTCGAACTCTGAGAGAGGCACTACGCGCGCTCCGCTGACAG	1070						
Db	4188430	GTTCTGAGATGACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4188489						
QY	1071	AAGTGCAGATTTTGTGAACACTCTGTTTACCGGCGCATTTGTTGCTGCGCT-----	1124						
Db	4188490	ACTGCGCGGCTTGGGAGCGCTTGTCTGACCGAGGATGCTGCTGCTGCTGCTGCTG	4188549						

QY 1125 -----GGGTTGGGCAATCACTTCTGAATCTTGATGATGTTGCTGCCAT 1175  
Db 4188550 CTCGTTGGGAGGCGTCAACCAATGCGCGATCCAGATCGAATCGAATCGAAGCAAC 4188609  
QY 1176 GAGTCCGCTGACGACCACTTAATTAATGCTTAACATGCGCGCAATTAATGCTGAGGCT 1235  
Db 4188610 GACCTGCGACCCCGGACATGCGCGTACCAATTCCTGCGGATGAGCGGCGCT 4188669  
QY 1236 CACCGACAGCGGCTTTCGAGTGGGTTTTCACGCGAGTGTCTTCGATTAATTTGCGGG 1295  
Db 4188670 GTCCGGGCTGTGCTGACGATCGAGCTATGCGCGCTTACGTTCTGTGCGCACCGCGG 4188729  
QY 1296 GCTTACTGCG--GCTGATGGTTCTGCGTTTATTAATCTTCTGTTTATTTAGGCC 1352  
Db 4188730 ACTCTGCGCGGACATGCGCGAATGCTGCTCATGCACTCGCGCGCGGCGGTTGCGCG 4188789  
QY 1353 CGTCTGCGCGGACGATGCTGCAACGAGTGTTCATCTGCTGTTTCTGTTGCTTCCGCG 1412  
Db 4188790 AGTGTGCGCACTCGAAGCCGCGGATGCGGCTTCTTGGCCACCTGATTTCAAT 4188849  
QY 1413 TCGATTTCTTAATTCACCGTTGATTTGCGATTTGCGGATTCACCAATGCTTCCAGG 1472  
Db 4188850 CCGTCCGAGGCTCCCGCTTGTGAGGCGACCGCGCATATGCGATGCTGCCGGG 4188909  
QY 1473 TCTAGCAATTTACCGCGAATGTAGCG--CACCTGATGATTAACACTCATGGGTTT 1529  
Db 4188910 CTTGCGGCTCTTCGTCGCGGTTTCGCTGATGACACACCGCGGCTCT 4188969  
QY 1530 CACCAATGTCGGGTTCTTTAGCCACGCTTCACTTGCAGCGCGCGGTTTGGG 1589  
Db 4188970 GACCCAGCTGTGAGAGCGCGCGACTGCACTGCGCTTGGACGCGGAGTGTGGG 4189029  
QY 1590 TGAAGTGGATTCG 1602  
Db 4189030 CGAGTTCTCGCC 4189042

RESULT 5  
US-08-232-463-14  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMM  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-9300  
TELEFAX: (703) 683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZapc-Fls  
US-08-232-463-14

Query Match  
Best Local Similarity 2.5%; Score 47.6; DB 1; Length 7218;  
Matches 14; Conservative 218; Mismatches 162; Indels 0; Gaps 0;

QY 1057 GCTCCGCTGACAGCAAGTGCAGATTTTTCGAAACCTCCTGTTTACCGCGGCAATGTT 1116  
Db 1042 GCTCAGAGTCGAGGAGCTTGCGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1101  
QY 1117 GCTGCGCTGGGTTGGGCAATTCAGCTTTGAAATCTTGATGATGATGCTGCGCATG 1176  
Db 1102 TTT 1161  
QY 1177 GAGTCCGCTGACAGCAAGTGCAGATTTTTCGTAACATTCGCGCATTAATGCGGCTC 1236  
Db 1162 TTT 1221  
QY 1237 ACGGACGCGCTTGCAGAGTGTGTTACGCGAGTGTCTCGATTAATGCGGAG 1296  
Db 1222 TTT 1281  
QY 1297 CTACGCGCTGATGGTTCTGCGTTTATTAATCTTCTGTTTATTAAGCCCGCTC 1356  
Db 1282 TTT 1341  
QY 1357 TCTGCGCTGCAATGCTGCAACAGAGTGTTCATGCTGATGCTGCTGCTGCGCGA 1416  
Db 1342 TTT 1401  
QY 1417 TCTGATTCACCGTGTGATGCGGATTCGCG 1450  
Db 1402 TTT 1435

RESULT 6  
US-08-956-171E-4234/C  
Sequence 4234, Application US/08956171E  
Patent No. 6593114  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
APPLICANT: Gil H. Choi  
APPLICANT: Patrick S. Dillon  
APPLICANT: Craig A. Rosen  
APPLICANT: Steven C. Barash  
APPLICANT: Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E

FILED DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 4234:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 400 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 4234:  
US-08-956-171E-4234

Query Match 2.4% Score 46.6; DB 4; Length 400;  
Best Local Similarity 61.9%; Pred. No. 9.8e-05;  
Matches 73; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 32 ATCCCCCCCCCTTGAAGCTGATGATTAATGAGCTGAGAGAGACTTGAACCTCAACTAC 91  
Db 298 AGCCCAATCGTTACCCCTCCATTAATGATGCGCGCCAGAGACTTGAAGCCCAACTAC 239  
QY 92 GCATTACAGAGCGCTTGGCGCTCCCAATGCGGCACCTCCAGCACCCCAATGCTGATGA 149  
Db 238 TGATTACAGTCAGTGTGCTTCAACCAATTGAGCTAGCGCGCTTAAGAAATGTTACGGA 181

RESULT 7  
US-09-198-452A-1  
Sequence 1, Application US/09198452A  
Patent No. 6559294  
GENERAL INFORMATION:  
APPLICANT: Grifflais, R.  
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
FILE REFERENCE: 9710-003-999  
CURRENT APPLICATION NUMBER: US/09/198,452A  
CURRENT FILING DATE: 1998-11-24  
NUMBER OF SEQ ID NOS: 6849  
SEQ ID NO 1230025  
LENGTH: 1230025  
TYPE: DNA  
ORGANISM: Chlamydia pneumoniae  
FEATURE:  
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Query Match 2.4%; Score 45.8; DB 4; Length 1230025;  
Best Local Similarity 76.7%; Pred. No. 0.033;  
Matches 56; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 61 GCTGAGAGAGAGACTTCACTCTCAACCTACGATTACAGTGCCTGCGCTGCAATTG 120  
Db 303710 GCTGAGAGAGAGAGACTTCACTCTCAACCTACGATTACAGTGCCTGCGCTGCAATTG 303769  
QY 121 CGCCACTCCAGCA 133  
Db 303770 AGCTACTCCAGCA 303782

RESULT 8  
US-08-956-171E-4023  
Sequence 4023, Application US/08956171E  
Patent No. 6593114  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
Gil H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 4023:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 381 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 4023:  
US-08-956-171E-4023

Query Match  
Best Local Similarity 73.1%; Pred. No. 0.0002;  
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

2.4%; Score 45.6; DB 4; Length 381;  
Best Local Similarity 73.1%; Pred. No. 0.0002;  
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 56 ATTGAGCTGGAGAGAGACTTGAACCTCTCAACCTAGCGATTACAGTGGCTGCTGCC 115  
DB 87 ATGAGNGNGCGGAGAGACTTGAACCCCAACCTAGTATTAACAAGTCTGCTTACC 146

QY 116 AATTGGCCCACTCCAGCA 133  
DB 147 AATTGAGCTAGCGCCGCA 164

RESULT 9  
US-08-956-171E-4566  
Sequence 4566, Application US/08956171E  
Patent No. 6593114  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
Gil H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 4566:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 237 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 4566:  
US-08-956-171E-4566

Query Match  
Best Local Similarity 73.1%; Pred. No. 0.00036;  
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

2.3%; Score 44.4; DB 4; Length 237;  
Best Local Similarity 73.1%; Pred. No. 0.00036;  
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 56 ATTGAGCTGGAGAGAGACTTGAACCTCTCAACCTAGCGATTACAGTGGCTGCTGCC 115  
DB 25 ATGTGTCGGCGGAGAGACTTGAACCCCAACCTAGTATTAACAAGTCTGCTTACC 84

QY 116 AATTGGCCCACTCCAGCA 133  
DB 85 AATTGAGCTAGCGCCGCA 102

RESULT 10  
US-08-956-171E-4543  
Sequence 4543, Application US/08956171E  
Patent No. 6593114  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
Gil H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 4543:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 4543:  
US-08-956-171E-4543

Query Match  
Best Local Similarity 73.1%; Pred. No. 0.00036;  
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

2.3%; Score 44.4; DB 4; Length 239;  
Best Local Similarity 73.1%; Pred. No. 0.00036;  
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 56 ATTGAGCTGGAGAGAGACTTGAACCTCTCAACCTAGCGATTACAGTGGCTGCTGCC 115  
DB 81 ATGTGTCGGCGGAGAGACTTGAACCCCAACCTAGTATTAACAAGTCTGCTTACC 140

QY 116 AATTGGCCCACTCCAGCA 133



Db 141 AATTGAGCTAGGCGCGCA 158

## RESULT 11

US-08-956-171E-4544

; Sequence 4544, Application US/08956171E

; Patent No. 6593114

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

; Gail H. Choi

; Patrick S. Dillon

; Craig A. Rosen

; Steven C. Barash

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5256

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/956,171E

; FILING DATE: 20-Oct-1997

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 60/009,861

; FILING DATE: January 5, 1996

; APPLICATION NUMBER: 08/781,986

; FILING DATE: January 3, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Mark J. Hyman

; REGISTRATION NUMBER: 46,789

; REFERENCE/DOCKET NUMBER: PB248P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (240) 314-1224

; TELEFAX: (301) 309-8439

; INFORMATION FOR SEQ ID NO: 4544:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 239 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 4544:

US-08-956-171E-4544

Query Match 2.3%; Score 44.4; DB 4; Length 239;

Best Local Similarity 73.1%; Pred. No. 0.00056;

Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 56 AATTGAGCTGAGAGAGACTTGAACCTCACTTACAGTGGCTGCGC 115

Db 72 ATGTGCGCGCGCAGAGAGACTTGAACCCCACTTACTGATTCAAGTCAAGTCTCTACC 131

QY 116 AATTGCGCACTCCAGCA 133

Db 132 AATTGAGCTAGGCGCGCA 149

RESULT 12

US-08-956-171E-3631

; Sequence 3631, Application US/08956171E

; Patent No. 6593114

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

; Gail H. Choi

; Patrick S. Dillon

; Craig A. Rosen

; Steven C. Barash

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5256

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 3631:

SEQUENCE CHARACTERISTICS:

LENGTH: 400 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3631:

US-08-956-171E-3631

Query Match 2.3%; Score 44.4; DB 4; Length 400;

Best Local Similarity 73.1%; Pred. No. 0.00056;

Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 56 AATTGAGCTGAGAGAGACTTGAACCTCACTTACAGTGGCTGCGC 115

Db 24 ATGTGCGCGCGCAGAGAGACTTGAACCCCACTTACTGATTCAAGTCAAGTCTCTACC 83

QY 116 AATTGCGCACTCCAGCA 133

Db 84 AATTGAGCTAGGCGCGCA 101

RESULT 13

US-08-956-171E-3660

; Sequence 3660, Application US/08956171E

; Patent No. 6593114

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

; Gail H. Choi

; Patrick S. Dillon

; Craig A. Rosen

; Steven C. Barash

; Michael R. Fannon

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5256

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 3660:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 400 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 3660:  
US-08-956-171E-3660

Query Match 2.3%; Score 44.4; DB 4; Length 400;  
Best Local Similarity 73.1%; Pred. No. 0.0005;  
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 56 ATTGAGCTGAGAGAGACTGTAACCTCAACCTACGATTAACAAGTGGCTGCC 115  
DB 20 ATGGTGGCGGCGAGAGACTGTAACCCCAACCTACGATTAACAAGTGGCTCAC 79  
QY 116 AATGGCGGCACTCCAGCA 133  
DB 80 AATTGAGCTAGCGCGGCA 97

## RESULT 14

US-08-956-171E-4198  
Sequence 4198, Application US/08956171E  
Patent No. 6593114  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
Gill H. Choi  
Patrick S. Dillon  
Steven C. Barash  
Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 4198:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 400 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 4198:  
US-08-956-171E-4198

Query Match 2.3%; Score 44.4; DB 4; Length 400;  
Best Local Similarity 73.1%; Pred. No. 0.0005;  
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 56 ATTGAGCTGAGAGAGACTGTAACCTCAACCTACGATTAACAAGTGGCTGCC 115  
DB 218 ATGGTGGCGGCGAGAGACTGTAACCCCAACCTACGATTAACAAGTGGCTCAC 277  
QY 116 AATGGCGGCACTCCAGCA 133  
DB 278 AATTGAGCTAGCGCGGCA 295

## RESULT 15

US-08-956-171E-4353  
Sequence 4353, Application US/08956171E  
Patent No. 6593114  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
Gill H. Choi  
Patrick S. Dillon  
Steven C. Barash  
Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789

```

/ REFERENCE/DOCKET NUMBER: PB248P1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (240) 314-1224
/ TELEFAX: (301) 309-8439
/ INFORMATION FOR SEQ ID NO: 4353:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 411 base pairs
/   TYPE: nucleic acid
/   STRANDEDNESS: double
/   TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4353:
US-08-956-171E-4353

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Query Match      2.3%; Score 44.4; DB 4; Length 411;
Best local Similarity 73.1%; Pred. No. 0.00051;
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 56 ATTGAGCTGGAGAGAGACTGTAACCTCAACCTACGATTACAAGTGGCTGGCC 115
   |||||
Db 183 ATGATGCCGGCCAGAGAGACTGGAACCCCAACTACTGATTACAAGTGGCTTACC 242
   |||||

QY 116 AATTGCGCCCACTCCAGCA 133
   |||||
Db 243 AATTGAGCTAGGCCGCGCA 260
   |||||

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-963-521-3

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Gapop 10.0 , Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:  
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16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
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19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1909	100.0	1909	9	US-09-951-536-3 Sequence 3, Appl1
2	1909	100.0	1909	9	US-09-963-521-3 Sequence 3, Appl1
3	1909	100.0	1909	9	US-09-834-721-3 Sequence 3, Appl1
4	1909	100.0	1909	9	US-09-783-388-3 Sequence 3, Appl1
5	1909	100.0	1909	9	US-09-951-535-3 Sequence 3, Appl1
6	1909	100.0	1909	10	US-10-224-574-11 Sequence 11, Appl1
7	1865.4	97.7	3309400	9	US-09-951-536-1 Sequence 1, Appl1
8	1836.6	96.2	2817	9	US-09-951-536-1 Sequence 1, Appl1
9	1836.6	96.2	2817	9	US-09-951-536-1 Sequence 1, Appl1
10	1836.6	96.2	2817	9	US-09-834-721-1 Sequence 1, Appl1
11	1836.6	96.2	2817	9	US-09-783-388-1 Sequence 1, Appl1
12	1836.6	96.2	2817	10	US-09-951-535-1 Sequence 1, Appl1
13	1836.6	96.2	2817	17	US-10-224-574-9 Sequence 9, Appl1
14	1590	83.3	1590	13	US-10-627-476-557 Sequence 55, App

15	1590	83.3	1590	13	US-10-450-055-41	Sequence 41, Appl1
16	1503	78.7	1503	9	US-09-738-626-2884	Sequence 2884, Ap
17	615.4	32.2	3010	14	US-10-058-945-1	Sequence 1, Appl1
18	188.8	9.9	2369	9	US-09-885-382-29	Sequence 29, Appl1
19	74.4	3.9	327	9	US-09-738-626-2885	Sequence 2885, Ap
20	46.6	2.4	400	8	US-08-781-986A-4234	Sequence 4234, Ap
21	46.6	2.4	400	13	US-10-329-624-4234	Sequence 4234, Ap
22	45.8	2.4	1061	13	US-10-027-632-324002	Sequence 324002,
23	45.8	2.4	1061	16	US-10-027-632-324002	Sequence 324002,
24	45.8	2.4	2955	17	US-10-437-963-89077	Sequence 89077, A
25	45.8	2.4	1230025	16	US-10-289-762-1	Sequence 1, Appl1
26	45.6	2.4	381	8	US-08-781-986A-4023	Sequence 4023, Ap
27	45.6	2.4	381	13	US-10-329-624-4023	Sequence 4023, Ap
28	44.8	2.3	194	17	US-10-437-963-23050	Sequence 23050, A
29	44.4	2.3	237	8	US-08-781-986A-4566	Sequence 4566, Ap
30	44.4	2.3	237	13	US-10-329-624-4566	Sequence 4566, Ap
31	44.4	2.3	239	8	US-08-781-986A-4543	Sequence 4543, Ap
32	44.4	2.3	239	13	US-10-329-624-4543	Sequence 4543, Ap
33	44.4	2.3	239	13	US-10-329-624-4543	Sequence 4543, Ap
34	44.4	2.3	239	13	US-10-329-624-4543	Sequence 4543, Ap
35	44.4	2.3	400	8	US-08-781-986A-3631	Sequence 3631, Ap
36	44.4	2.3	400	8	US-08-781-986A-3660	Sequence 3660, Ap
37	44.4	2.3	400	8	US-08-781-986A-4198	Sequence 4198, Ap
38	44.4	2.3	400	13	US-10-329-624-3631	Sequence 3631, Ap
39	44.4	2.3	400	13	US-10-329-624-3660	Sequence 3660, Ap
40	44.4	2.3	400	13	US-10-329-624-4198	Sequence 4198, Ap
41	44.4	2.3	411	8	US-08-781-986A-4353	Sequence 4353, Ap
42	44.4	2.3	411	13	US-10-329-624-4353	Sequence 4353, Ap
43	44.4	2.3	475	8	US-08-781-986A-3621	Sequence 3621, Ap
44	44.4	2.3	475	13	US-10-329-624-3621	Sequence 3621, Ap
45	44.4	2.3	6591	8	US-08-781-986A-3114	Sequence 3114, Ap

## ALIGNMENTS

RESULT 1  
US-09-951-536-3  
Sequence 3, Application US/09951536  
Patent No. US20020107378A1  
GENERAL INFORMATION:  
APPLICANT: ZIEGLER, PETRA  
APPLICANT: BEGELING, LOTMAR  
APPLICANT: SAMM, HERMANN  
APPLICANT: THIERBACH, GEORG  
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND  
TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE  
FILE REFERENCE: 21123/282414/MAS  
CURRENT APPLICATION NUMBER: US/09/951,536  
CURRENT FILING DATE: 2001-09-14  
PRIOR APPLICATION NUMBER: 09/431,099  
PRIOR FILING DATE: 1999-11-01  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 1909  
TYPE: DNA  
ORGANISM: Corynebacterium glutamicum  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (280)..(1746)  
OTHER INFORMATION: thre-Gen  
US-09-951-536-3

Query Match 100.0%; Score 1909; DB 9; Length 1909;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTGCATCCTGCAGAGTGCAGCTAGAGATCCCGCCCTTGACCGGTTATTGA 60  
DB 1 AGCTTGCATCCTGCAGAGTGCAGCTAGAGATCCCGCCCTTGACCGGTTATTGA 60

QY	61	GCTGGAGAAAGACTTGAATCTTCACCACTTACGATTTACAAAGCGCTTGGCGCAATTG	120
Db	61	GCTGGAGAAAGACTTGAATCTTCACCACTTACGATTTACAAAGCGCTTGGCGCAATTG	120
QY	121	CGGCACATCCAGCACCGGAGATGCTGATGATCAACAATCAGATACGATCTTAAAGGAT	180
Db	121	CGGCACATCCAGCACCGGAGATGCTGATGATCAACAATCAGATACGATCTTAAAGGAT	180
QY	181	GTTGATCATCAATGGAATTCGGGGCTAAGATCTGTGTGAACCGTGCATTAACGACCTG	240
Db	181	GTTGATCATCAATGGAATTCGGGGCTAAGATCTGTGTGAACCGTGCATTAACGACCTG	240
QY	241	TGATTTGACCTTTTCTTCTTGCAAAAATGTTTTCAAGGGATGTTGAGTTTTGGAACCTT	300
Db	241	TGATTTGACCTTTTCTTCTTGCAAAAATGTTTTCAAGGGATGTTGAGTTTTGGAACCTT	300
QY	301	CGTGGCGCATTTTCAACAGATTGACGCTGTCAAAACCGCACCTTCGCCATTCGCACTAAGC	360
Db	301	CGTGGCGCATTTTCAACAGATTGACGCTGTCAAAACCGCACCTTCGCCATTCGCACTAAGC	360
QY	361	CCGATTTGATCTCACTGACACATATGTCAGATGGCGGGTGTATGTAATTTGGCTGCGAATTT	420
Db	361	CCGATTTGATCTCACTGACACATATGTCAGATGGCGGGTGTATGTAATTTGGCTGCGAATTT	420
QY	421	GGCATAATTTTGCCTTCTTTCAGTACGTCAATATGTGACA CAAAGTACAAAGTTTCAACA	480
Db	421	GGCATAATTTTGCCTTCTTTCAGTACGTCAATATGTGACA CAAAGTACAAAGTTTCAACA	480
QY	481	GTGACCTCTGGTACGAGCTTTGTACTACACGACGCTGATATACGTTGATATGATACAC	540
Db	481	GTGACCTCTGGTACGAGCTTTGTACTACACGACGCTGATATACGTTGATATGATACAC	540
QY	541	ATCTTCACCAACATCGATGTGTGAGAGAGAGATGCGGTCAACGCTGTTCAATGTTTGAAGC	600
Db	541	ATCTTCACCAACATCGATGTGTGAGAGAGAGATGCGGTCAACGCTGTTCAATGTTTGAAGC	600
QY	601	AAATTGGAACACCACTTCTCCAACTGTCTTGAAGTTGACCGTGTGATCCGTTCCATTCAG	660
Db	601	AAATTGGAACACCACTTCTCCAACTGTCTTGAAGTTGACCGTGTGATCCGTTCCATTCAG	660
QY	661	GCTGGTGGAGACCCCGCTGAGGTTGCGCAGAAAATCTCGACGAGTTGAGCAATCCCT	720
Db	661	GCTGGTGGAGACCCCGCTGAGGTTGCGCAGAAAATCTCGACGAGTTGAGCAATCCCT	720
QY	721	GCGTCTTAATGTTTTCCCTGTTGCGTTGCTGTGCGTGTGCGATGATGGTGCTGTTGCT	780
Db	721	GCGTCTTAATGTTTTCCCTGTTGCGTTGCTGTGCGTGTGCGATGATGGTGCTGTTGCT	780
QY	781	GTGCTGTTGGGTGTGGATGAGCAGGTTTCCCTAATGTGTTTTATTAACGAGTTACGATC	840
Db	781	GTGCTGTTGGGTGTGGATGAGCAGGTTTCCCTAATGTGTTTTATTAACGAGTTACGATC	840
QY	841	ATTGCGACAGACGTCAATTTTGGGAAAGAGGGTTGCTCACTTTCCTTCAAAATGTTGTT	900
Db	841	ATTGCGACAGACGTCAATTTTGGGAAAGAGGGTTGCTCACTTTCCTTCAAAATGTTGTT	900
QY	901	GGTGGTTTTATTTGCGACAGCTGCTTCGATCGATGCTTTATCTTTGGCGTTGCAATTTGGT	960
Db	901	GGTGGTTTTATTTGCGACAGCTGCTTCGATCGATGCTTTATCTTTGGCGTTGCAATTTGGT	960
QY	961	CTTGGATCAAAACCGAGCAGATTCATCGCATCTGGAAATTTGTTGTGCTTGGCAGGTTTG	1020
Db	961	CTTGGATCAAAACCGAGCAGATTCATCGCATCTGGAAATTTGTTGTGCTTGGCAGGTTTG	1020
QY	1021	ACACTGTCGAATCTCTCGACAGACCGCATCAAGGGCGCTCGGTGACGACAAGTGCACGA	1080
Db	1021	ACACTGTCGAATCTCTCGACAGACCGCATCAAGGGCGCTCGGTGACGACAAGTGCACGA	1080
QY	1081	TTTTTGGAAACCTCTCTGTTTACCGGCGGCAATTTGTTGCTGGGTGGGTTTGGCAATTCAG	1140
Db	1081	TTTTTGGAAACCTCTCTGTTTACCGGCGGCAATTTGTTGCTGGGTGGGTTTGGCAATTCAG	1140
QY	1141	CTTTCGAAATCTTGCAATTCATGTTGCTGCAATGAGTCCGCTGCACGACTTAATTTAT	1200

Db	1141	CTTTGGAATCTTGATGTCATGATGTCCTGCGCATGAGTCCTGACGACCTAATTAT	1200
Qy	1201	TCGCTACATTCGCGCGCATTAATCGCTGATGGCGTCAACGACGGGACCTTGCAATGGGT	1260
Db	1201	TGCTCTACATTCGCGCGCATTAATCGCTGATGGCGTCAACGACGGGACCTTGCAATGGGT	1260
Qy	1261	TGTTACGGGAGTGTCTCTGGTGAATATTATGCGGGGCTTACTGGCGTGAATGGGTCTGGC	1320
Db	1261	TGTTACGGGAGTGTCTCTGGTGAATATTATGCGGGGCTTACTGGCGTGAATGGGTCTGGC	1320
Qy	1321	TTTTATTAACCTCTGCTGTTTATTTATGAGCCCGGCTCTGGCGCGTGCAGATTCGCAACA	1380
Db	1321	TTTTATTAACCTCTGCTGTTTATTTATGAGCCCGGCTCTGGCGCGTGCAGATTCGCAACA	1380
Qy	1381	GCAATGTTTCACTGATGTTTGTCTGACCCGCGATTCCTTGAATTCACCGTTGATTGTG	1440
Db	1381	GCAATGTTTCACTGATGTTTGTCTGACCCGCGATTCCTTGAATTCACCGTTGATTGTG	1440
Qy	1441	GCGAATCCCGGCAATCAACCAATCTTCAGATCTAGCAATTTACCGGGAAATGAAGGC	1500
Db	1441	GCGAATCCCGGCAATCAACCAATCTTCAGATCTAGCAATTTACCGGGAAATGAAGGC	1500
Qy	1501	ACCGTGAATATCAACACTATGAGGTTTTCAACAATTCGCGGTGCTTATGACCACTGCT	1560
Db	1501	ACCGTGAATATCAACACTATGAGGTTTTCAACAATTCGCGGTGCTTATGACCACTGCT	1560
Qy	1561	TCATCACTTGGCGCGTGGCGTGGTATTTGGGTGATGGATTTGCCCGAGGCTACGTGTCOA	1620
Db	1561	TCATCACTTGGCGCGTGGCGTGGTATTTGGGTGATGGATTTGCCCGAGGCTACGTGTCOA	1620
Qy	1621	CCACGCTTCAACCCATACCGTGCATTTTACCAAGCGCATTGATGTTCTCTCCAGAGAGAA	1680
Db	1621	CCACGCTTCAACCCATACCGTGCATTTTACCAAGCGCATTGATGTTCTCTCCAGAGAGAA	1680
Qy	1681	GCTAGAGCAATCAAGCGCGCGCAGAGAAACGTCACAAAGCTAATACAGATTCGATAT	1740
Db	1681	GCTAGAGCAATCAAGCGCGCGCAGAGAAACGTCACAAAGCTAATACAGATTCGATAT	1740
Qy	1741	AAAAGTAAAAAATCAACCTGCTTAGGCGTCTTTGCTTAAATAGCGTAGAATATGGGTC	1800
Db	1741	AAAAGTAAAAAATCAACCTGCTTAGGCGTCTTTGCTTAAATAGCGTAGAATATGGGTC	1800
Qy	1801	GATGCGCTTTTAAACACTAGAGAGATCTCTGCGCGCAAAATACAGACACTGTCGCCAC	1860
Db	1801	GATGCGCTTTTAAACACTAGAGAGATCTCTGCGCGCAAAATACAGACACTGTCGCCAC	1860
Qy	1861	CCGAGAAATCCCTTACGCTGTGAAAGAGAAACCGCAGCGGGGATACCG	1909
Db	1861	CCGAGAAATCCCTTACGCTGTGAAAGAGAAACCGCAGCGGGGATACCG	1909

RESULT 2

US-09-963-521-3

; Sequence 3, Application US/09963521

; Patent No. US20020146781A1

; GENERAL INFORMATION:

; APPLICANT: ZIEGLER, PETRA

; APPLICANT: EGGELING, IOTHAR

; APPLICANT: SAHM, HERMANN

; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE

; TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF

; FILE REFERENCE: 21123/282413/MAS

; CURRENT APPLICATION NUMBER: US/09/963,521

; PRIOR FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: 09/431,099

; PRIOR FILING DATE: 1999-11-01

; PRIOR APPLICATION NUMBER: DE 199 41 478.5

; PRIOR FILING DATE: 1999-09-01

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

LENGTH: 1909  
TYPE: DNA  
ORGANISM: Corynebacterium glutamicum  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (280)..(1746)  
OTHER INFORMATION: thre-Gen  
US-09-963-521-3

Query Match 100.0%; Score 1909; DB 9; Length 1909;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTGATGCTCTGAGTGTGATCTTGAGGATCCCCCTTTGACCTGCTGTTATGA 60  
Db 1 AGCTTGATGCTCTGAGTGTGATCTTGAGGATCCCCCTTTGACCTGCTGTTATGA 60  
QY 61 GCTGAGAGAGAGATTGAACTCTGACCTTCAAGTTCAGAGTTCAGGATTCGCTGCAATTG 120  
Db 61 GCTGAGAGAGAGATTGAACTCTGACCTTCAAGTTCAGAGTTCAGGATTCGCTGCAATTG 120  
QY 121 CGCCTCTCCAGCAACCGGAGATGCTGATGATCAACAACTAATACCTATCTTACGCTAT 180  
Db 121 CGCCTCTCCAGCAACCGGAGATGCTGATGATCAACAACTAATACCTATCTTACGCTAT 180  
QY 181 GTGTACATCAATGGAATTCGGGGCTAGAGTATCTGTGAACCGTGCATTAACGACCTG 240  
Db 181 GTGTACATCAATGGAATTCGGGGCTAGAGTATCTGTGAACCGTGCATTAACGACCTG 240  
QY 241 TGATGGACTCTTTCTTCTGCAAAATGTTTCCAGCGGAGTGTGAGTTCGCAACCTT 300  
Db 241 TGATGGACTCTTTCTTCTGCAAAATGTTTCCAGCGGAGTGTGAGTTCGCAACCTT 300  
QY 301 CGTGGCGGCAATTTCAACAGTTGACGCTGCAAAACCGGCACTCCGCAATCGCACTAGCC 360  
Db 301 CGTGGCGGCAATTTCAACAGTTGACGCTGCAAAACCGGCACTCCGCAATCGCACTAGCC 360  
QY 361 CGGATGATCTCACTGACCACTAGTCAAGTGGCGGCTGATGATTTGGCTGCGAGATT 420  
Db 361 CGGATGATCTCACTGACCACTAGTCAAGTGGCGGCTGATGATTTGGCTGCGAGATT 420  
QY 421 GGGGATATTTTCTTCTTCTGAGTACGTCATATAGTACACAGGAGTCAAGTTCCAGCA 480  
Db 421 GGGGATATTTTCTTCTTCTGAGTACGTCATATAGTACACAGGAGTCAAGTTCCAGCA 480  
QY 481 GTGACCTCTGCGATGCGGTTGTACTACAGCACTGGAATATCAAGTTGAATACGATCAC 540  
Db 481 GTGACCTCTGCGATGCGGTTGTACTACAGCACTGGAATATCAAGTTGAATACGATCAC 540  
QY 541 ATCTTCACCAACATCGGCTGTGAGAGAGAGATGCCGCTCAACGCTGTTGATGTTAGGC 600  
Db 541 ATCTTCACCAACATCGGCTGTGAGAGAGAGATGCCGCTCAACGCTGTTGATGTTAGGC 600  
QY 601 AAGTTGAGACCAACTCTTCCAACTGTCTGAGTTCGACCGTTGATCCGTTCCATTGACG 660  
Db 601 AAGTTGAGACCAACTCTTCCAACTGTCTGAGTTCGACCGTTGATCCGTTCCATTGACG 660  
QY 661 GCTGTGAGACCCCGCTGAGGTTGCCGAGAAATCTGACGAGTTGAGACATCCCTT 720  
Db 661 GCTGTGAGACCCCGCTGAGGTTGCCGAGAAATCTGACGAGTTGAGACATCCCTT 720  
QY 721 GGGCTTAATGTTTCCCTGTTGGCTGCTTGGGCAATGATGAGTGTGCTGTTGCT 780  
Db 721 GGGCTTAATGTTTCCCTGTTGGCTGCTTGGGCAATGATGAGTGTGCTGTTGCT 780  
QY 781 GTGCTGTTGGTGTGATGAGGATGCTTCCATATGCTTTATTAACGCGTTCCAGATC 840  
Db 781 GTGCTGTTGGTGTGATGAGGATGCTTCCATATGCTTTATTAACGCGTTCCAGATC 840  
QY 841 ATTGCGACAGCTCATTTTGGAGAAAGAGGTTGCTTCTTCCAAATGTTGT 900  
Db 841 ATTGCGACAGCTCATTTTGGAGAAAGAGGTTGCTTCTTCCAAATGTTGT 900

QY 901 GGTGTTTTATTTGCGACGCTCCGTCATTCGATTCCTTATTTCTTGGGCTTGCAATTTGT 960  
Db 901 GGTGTTTTATTTGCGACGCTCCGTCATTCGATTCCTTATTTCTTGGGCTTGCAATTTGT 960  
QY 961 CTTGAGATCAACCGAGCCGATATATGCACTTGGAATTTGTTGCTGTTGGCAGTTTG 1020  
Db 961 CTTGAGATCAACCGAGCCGATATATGCACTTGGAATTTGTTGCTGTTGGCAGTTTG 1020  
QY 1021 AACTGCTGCAATCTCTGAGAGACGGATCAACGGGCGCTCCGGGACAGACAGTGCACGA 1080  
Db 1021 AACTGCTGCAATCTCTGAGAGACGGATCAACGGGCGCTCCGGGACAGACAGTGCACGA 1080  
QY 1081 TTTTTCGAAACACTCTGTTTACCGGCGGATTTGCTGCGGCTTGGGCTTGGCATTCAG 1140  
Db 1081 TTTTTCGAAACACTCTGTTTACCGGCGGATTTGCTGCGGCTTGGGCTTGGCATTCAG 1140  
QY 1141 CTTTCTGAATCTTTCATGTCATGTTGCTGCGATGAGTTCGCTGACGACCTAATAT 1200  
Db 1141 CTTTCTGAATCTTTCATGTCATGTTGCTGCGATGAGTTCGCTGACGACCTAATAT 1200  
QY 1201 TCGCTACATTTGGCGGCAATTTATGCTGCTGCTGCTGCAACGGAGGCTTTCGCACTGGGT 1260  
Db 1201 TCGCTACATTTGGCGGCAATTTATGCTGCTGCTGCTGCAACGGAGGCTTTCGCACTGGGT 1260  
QY 1261 TGTACGCGAGTGTCTCTGCTGATTAATTCGCGGCTTACTGCGCTGATGAGTTCTGCG 1320  
Db 1261 TGTACGCGAGTGTCTCTGCTGATTAATTCGCGGCTTACTGCGCTGATGAGTTCTGCG 1320  
QY 1321 TTTTATTAACCTCTTCTGTTTATTAAGCCCGGCTCTGCGCTGCGATTCGTCACAA 1380  
Db 1321 TTTTATTAACCTCTTCTGTTTATTAAGCCCGGCTCTGCGCTGCGATTCGTCACAA 1380  
QY 1381 GCACTGCTTCACTGCGGCTTTCGCTGCGCGGCTGCTGCTGATTCACCGGATTCGTG 1440  
Db 1381 GCACTGCTTCACTGCGGCTTTCGCTGCGCGGCTGCTGCTGATTCACCGGATTCGTG 1440  
QY 1441 GCGATTGCGGCAATCAACCAATGCTTCCAGTCTGACATTTTACCGCGGAATGTAGCC 1500  
Db 1441 GCGATTGCGGCAATCAACCAATGCTTCCAGTCTGACATTTTACCGCGGAATGTAGCC 1500  
QY 1501 ACCCTGAATGATTAACACTGATGCTTTCACCAATTTGCGGCTTTCACCACTGCT 1560  
Db 1501 ACCCTGAATGATTAACACTGATGCTTTCACCAATTTGCGGCTTTCACCACTGCT 1560  
QY 1561 TCATCACTTCCGCTGCGGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620  
Db 1561 TCATCACTTCCGCTGCGGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620  
QY 1621 CCAAGCTTCAACCCATACCGTGCATTTTACCAAGGCGAATGATTCCTTCCAGAGAA 1680  
Db 1621 CCAAGCTTCAACCCATACCGTGCATTTTACCAAGGCGAATGATTCCTTCCAGAGAA 1680  
QY 1681 GCTGAGCAATCAAGGCGGCGGAGAGAAAGTCCAAAGCTATATAGATTCGGTAAT 1740  
Db 1681 GCTGAGCAATCAAGGCGGCGGAGAGAAAGTCCAAAGCTATATAGATTCGGTAAT 1740  
QY 1741 AAAAGTAAATCAACTGCTTACGCTCTTTCGTTAAATAGCTAATATGCGGCTC 1800  
Db 1741 AAAAGTAAATCAACTGCTTACGCTCTTTCGTTAAATAGCTAATATGCGGCTC 1800  
QY 1801 GATCGCTTTTAAACACTGAGAGGATCTTTCGCGGCAAAATCAAGGACACTGCTCCAC 1860  
Db 1801 GATCGCTTTTAAACACTGAGAGGATCTTTCGCGGCAAAATCAAGGACACTGCTCCAC 1860  
QY 1861 CCGAGATCCCTCAAGCTGTTGAAGAGAAACCGGAGCGGGGATACCG 1909  
Db 1861 CCGAGATCCCTCAAGCTGTTGAAGAGAAACCGGAGCGGGGATACCG 1909

RESULT 3  
US-09-834-721-3  
; Sequence 3, Application US/09834721  
; Patent No. US2002015551A1







Db 1561 TCATCACTGCGGCTGCGCTGTTTGGGTAGTGAATGCCGACGCTACGCTCCA 1620  
QY 1621 CCACGCTTCAACCCATACCGCTGCAATTAACAGGCGAATGATTTCTCTCCAGAGGAA 1680  
Db 1621 CCACGCTTCAACCCATACCGCTGCAATTAACAGGCGAATGATTTCTCTCCAGAGGAA 1680  
QY 1681 GCTGAGCAATAGAGCGCGCGAGAGAAAGCTCCAAAGACTAATCAGAGATTCGGTAT 1740  
Db 1681 GCTGAGCAATAGAGCGCGCGAGAGAAAGCTCCAAAGACTAATCAGAGATTCGGTAT 1740  
QY 1741 AAAAGGTAATCAACCTGCTTAGGCGCTTTGCTTAATAGCGTAGAATATCGGGTC 1800  
Db 1741 AAAAGGTAATCAACCTGCTTAGGCGCTTTGCTTAATAGCGTAGAATATCGGGTC 1800  
QY 1801 GATGCTTTTAAACACTCAGAGAGATCTTCCGCGCAAAATCAGGACACTGCTCCAC 1860  
Db 1801 GATGCTTTTAAACACTCAGAGAGATCTTCCGCGCAAAATCAGGACACTGCTCCAC 1860  
QY 1861 CCCAGATCCCTTACGCTGTGAAGAGAAACCGGACCGGGGTACCG 1909  
Db 1861 CCCAGATCCCTTACGCTGTGAAGAGAAACCGGACCGGGGTACCG 1909

## RESULT 5

US-09-951-535-3

; Sequence 3, Application US/09951535  
; Publication No. US20030049802A1

; GENERAL INFORMATION:

; APPLICANT: ZIEGLER, PETRA

; APPLICANT: EISELING, LOTHAR

; APPLICANT: SAHM, HERMANN

; APPLICANT: THERBACH, GEORG

; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND  
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE

; FILE REFERENCE: 21123/282415/MAS

; CURRENT APPLICATION NUMBER: US/09/951,535

; PRIOR FILING DATE: 2001-09-14

; PRIOR APPLICATION NUMBER: 09/431,099

; PRIOR FILING DATE: 1999-11-01

; PRIOR APPLICATION NUMBER: DE 199 41 478.5

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 1909

; TYPE: DNA

; ORGANISM: Corynebacterium glutamicum

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (280)..(1746)

; OTHER INFORMATION: ltrE-Gen

US-09-951-535-3

Query Match 100.0%; Score 1909; DB 10; Length 1909;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTGATGCTCTGAGGTGCACTGTAGAGATCCCCCTTTTACCTGCTGTTATTGA 60  
Db 1 AGCTTGATGCTCTGAGGTGCACTGTAGAGATCCCCCTTTTACCTGCTGTTATTGA 60  
QY 61 GCTGAGAGAGACTTGAATCTCAACCTTACAGATTAAGAGCGTGGCGCAATTG 120  
Db 61 GCTGAGAGAGACTTGAATCTCAACCTTACAGATTAAGAGCGTGGCGCAATTG 120  
QY 121 GCGCACTCAGACCGCAGATGCTATGATCAACAACCTACGAAATGATCTTAGGAT 180  
Db 121 GCGCACTCAGACCGCAGATGCTATGATCAACAACCTACGAAATGATCTTAGGAT 180  
QY 181 GTGTACATCAATGAAATTCGGGGCTAGAGTATCTGTGAACGCTGATTAACGACTG 240  
Db 181 GTGTACATCAATGAAATTCGGGGCTAGAGTATCTGTGAACGCTGATTAACGACTG 240

QY	1321	TTTTATATACCTTCTGTTGTTATTATTAGGCCCGCTCTGCGCGTGGATTGTGCACAA	1380
Db	1321	TTTTATATACCTTCTGTTGTTATTATTAGGCCCGCTCTGCGCGTGGATTGTGCACAA	1380
QY	1381	GCAGTTGGTTTCACTCGTGGTTGCTTGGCCCGCGAATTCCTGATTCACACGTTGATTGTG	1440
Db	1381	GCAGTTGGTTTCACTCGTGGTTGCTTGGCCCGCGAATTCCTGATTCACACGTTGATTGTG	1440
QY	1441	GGCATTTGCCGGCATCACACCAATGCTTCCAGAGCTTAGCAATTAACCGCGAATGTACGCC	1500
Db	1441	GGCATTTGCCGGCATCACACCAATGCTTCCAGAGCTTAGCAATTAACCGCGAATGTACGCC	1500
QY	1501	ACCGTGAATGATTCAAACAACACTATGGGTTTCCACCAACTTGGCGGTTGCTTAAGCCACTGCT	1560
Db	1501	ACCGTGAATGATTCAAACAACACTATGGGTTTCCACCAACTTGGCGGTTGCTTAAGCCACTGCT	1560
QY	1561	TCATCACTGTCGCGTGGCGTGGTTTGGGTGGAGTGGATTGGCCCGAGGCTTACGTCCCA	1620
Db	1561	TCATCACTGTCGCGTGGCGTGGTTTGGGTGGAGTGGATTGGCCCGAGGCTTACGTCCCA	1620
QY	1621	CCACGCTTCAAACCCATACCGTGATTTTACCAAGCGCAATGATTCCTTCCAGAGAGAA	1680
Db	1621	CCACGCTTCAAACCCATACCGTGATTTTACCAAGCGCAATGATTCCTTCCAGAGAGAA	1680
QY	1681	GGTGAAGAGAAATTCAGCGCGCGGACAGAAACGTCCTCAAGACTATATCAGAGATTCCGTAAT	1740
Db	1681	GGTGAAGAGAAATTCAGCGCGCGGACAGAAACGTCCTCAAGACTATATCAGAGATTCCGTAAT	1740
QY	1741	AAAAAGTAAAAATCAACCTGCTTAGGCGCTTCTGCTTAATAGGTAGTAATTCGGGTC	1800
Db	1741	AAAAAGTAAAAATCAACCTGCTTAGGCGCTTCTGCTTAATAGGTAGTAATTCGGGTC	1800
QY	1801	GATGCTTTTAAACACTCAGAGAGATCCTTGGCCGCCAAATCAGCGACACTGTCAC	1860
Db	1801	GATGCTTTTAAACACTCAGAGAGATCCTTGGCCGCCAAATCAGCGACACTGTCAC	1860
QY	1861	CCGAGATTCCTCTTACGCTGTGTGAAGAGAGAAACCGACGCGGAGTACCG	1909
Db	1861	CCGAGATTCCTCTTACGCTGTGTGAAGAGAGAAACCGACGCGGAGTACCG	1909

RESULT 6  
US-10-224-574-11  
; Sequence 11, Application US/10224574  
; Publication No. US20040101837A1  
; GENERAL INFORMATION:  
; APPLICANT: Forschungszentrum Jlich GmbH, P. Ziegler, L. Eggeling, H. Sahm,  
; APPLICANT: P. Peters- Wendsch  
; TITLE OF INVENTION: Nucleotide sequences coding for proteins participating in the SYN  
; TITLE OF INVENTION: L-serin, improved process for the microbial manufacture of L-ser  
; TITLE OF INVENTION: genetically modified microorganism suitable for the process.  
; FILE REFERENCE: FZJ-9912-PCR  
; CURRENT APPLICATION NUMBER: US/10/224,574  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 1909  
; TYPE: DNA  
; ORGANISM: C. glutamicum ATCC 13 032  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (280)..(1746)  
; OTHER INFORMATION: thr E (Threonin-exportcarrier)  
US-10-224-574-11

	Query Match	100.0%	Score 1909	DB 17	Length 1909
	Best Local Similarity	100.0%	Pred. No. 0		
	Matches 1909	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qx	1	AGCTTGACAGCTGAGGTGACCTCTAGAGGATCCCCCCTTTGACCTGCTGTTATGA	60		
Db	1	AGCTTGACAGCTGAGGTGACCTCTAGAGGATCCCCCCTTTGACCTGCTGTTATGA	60		

[illegible]

QY	1141	CTTTCGAAATCTTGATGTCATGTTGCTGCGCATGAGTCCGCTGACAGCACTTAATTAT	1200
Db	1141	CTTTCGAAATCTTGATGTCATGTTGCTGCGCATGAGTCCGCTGACAGCACTTAATTAT	1200
QY	1201	TGCTGTAACTTGGCCGSCATTTATTCGCGTGGTGGGCTACCCGACGGGCTTCGAGTGGGT	1260
Db	1201	TGCTGTAACTTGGCCGSCATTTATTCGCGTGGTGGGCTACCCGACGGGCTTCGAGTGGGT	1260
QY	1261	TGTTACGCGAGTGGTCCCTCGGTGATTTATTCGCGGCTTACTGCGCTGATGGGTTCTGGG	1320
Db	1261	TGTTACGCGAGTGGTCCCTCGGTGATTTATTCGCGGCTTACTGCGCTGATGGGTTCTGGG	1320
QY	1321	TTTTATTACCTCTTCGTTGTTTATTTATAGGCCCGCTCTCTGCGCTGGATTCGTCACAA	1380
Db	1321	TTTTATTACCTCTTCGTTGTTTATTTATAGGCCCGCTCTCTGCGCTGGATTCGTCACAA	1380
QY	1381	GCAGTTGGTTTCACTGGTGGTTTGCTTGGCGCGTGGATTCTTGATTCACCGTTGATTTGTG	1440
Db	1381	GCAGTTGGTTTCACTGGTGGTTTGCTTGGCGCGTGGATTCTTGATTCACCGTTGATTTGTG	1440
QY	1441	GCAGTTCCGCGCATCACACCAATGCTTCAAGCTTACCAATTTACCGCGAGATGTACGCC	1500
Db	1441	GCAGTTCCGCGCATCACACCAATGCTTCAAGGTTACCAATTTACCGCGAGATGTACGCC	1500
QY	1501	ACCCTGAATGATCAACAACATCATGAGGTTTACCAAACTATGGGTTGCTTTAGCCACTGCT	1560
Db	1501	ACCCTGAATGATCAACAACATCATGAGGTTTACCAAACTATGGGTTGCTTTAGCCACTGCT	1560
QY	1561	TCATCACTTGGCGCTGGCGGTGTTTGGGTGAGTGGATTTGCCCGAGGCTTACGTCTCCA	1620
Db	1561	TCATCACTTGGCGCTGGCGGTGTTTGGGTGAGTGGATTTGCCCGAGGCTTACGTCTCCA	1620
QY	1621	CCAGGCTTCAACCATACCTGTCATTTTACCAAGCGAATGATTTCTCTTCAGAGAGAA	1680
Db	1621	CCAGGCTTCAACCATACCTGTCATTTTACCAAGCGAATGATTTCTCTTCAGAGAGAA	1680
QY	1681	GCTGAGCAGAAATCAGCGCGCGCAGAGAAAAGCTCCAAAAGCTAATCAGAGTTGGTAT	1740
Db	1681	GCTGAGCAGAAATCAGCGCGCGCAGAGAAAAGCTCCAAAAGCTAATCAGAGTTGGTAT	1740
QY	1741	AAAAGTAAAAATCAACTGCTTGGGCGCTTTGGCTTAAADAGGATGAAATCGGGTC	1800
Db	1741	AAAAGTAAAAATCAACTGCTTGGGCGCTTTGGCTTAAADAGGATGAAATCGGGTC	1800
QY	1801	GATGCTTTTAAACACTCAGAGAGATCTTTCGCGGCAAAATCAGCACTGTCAC	1860
Db	1801	GATGCTTTTAAACACTCAGAGAGATCTTTCGCGGCAAAATCAGCACTGTCAC	1860
QY	1861	CCCAAAATCCTTCAACGCTGTTGAAGAGAAAACGCGACCGGGGTATCGG	1909
Db	1861	CCCAAAATCCTTCAACGCTGTTGAAGAGAAAACGCGACCGGGGTATCGG	1909
RESULT 7			
US-09-738-626-1			
; Sequence 1, Application US/09738626			
; Publication No. US20020197605A1			
; GENERAL INFORMATION:			
; APPLICANT: NAKAGAWA, SATOSHI			
; APPLICANT: MIZOGUCHI, HIROSHI			
; APPLICANT: ANDO, SEIKO			
; APPLICANT: HAYASHI, MIKIRO			
; APPLICANT: OCHIAI, KEIKO			
; APPLICANT: YOKOI, HARUHIKO			
; APPLICANT: TATEISHI, NAOKO			
; APPLICANT: SENOH, AKIHIRO			
; APPLICANT: IKEDA, MASATO			
; APPLICANT: OZAKI, AKIO			
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES			
; FILE REFERENCE: 249-125			
; CURRENT APPLICATION NUMBER: US/09/738, 626			
; CURRENT FILING DATE: 2000-12-18			
; PRIOR APPLICATION NUMBER: JP 99/377484			

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? PRIOR FILLING DATE: 1999-12-16
? PRIOR APPLICATION NUMBER: JP 00/159160
? PRIOR FILLING DATE: 2000-04-07
? PRIOR APPLICATION NUMBER: JP 00/280988
? PRIOR FILLING DATE: 2000-08-03
? NUMBER OF SEQ ID NOS: 7059
? SOFTWARE: PatentIn ver. 3.0
? SEQ ID NO: 1
? LENGTH: 3309400
? TYPE: DNA
? ORGANISM: Corynebacterium glutamicum
? US-09-738-626-1

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Query Match	97.7%	Score 1865.4;	DB 9;	Length 3309400;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1866;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

QY	38	CCGCTTTGACCTGGGCTTATTTGAGCTGGAGAAAGAACTTGAACCTCTCAACCTAGACATTA	97
Db	2790740	CCCTTTGACCTGGGCTTATTTGAGCTGGAGAAAGAACTTGAACCTCTCAACCTAGACATTA	2790799
QY	98	CAAGTGCATTTGGCGCTGCATTTGGCCACTCCAGCACCGAGATCTGATGATCAACAC	157
Db	2790800	CAAGTGCATTTGGCGCTGCATTTGGCCACTCCAGCACCGAGATCTGATGATCAACAC	2790859
QY	158	TACGAATACGATCTTAAAGGCTATGTGTACATTCACAAATGGAAATTTGGGGCTGAGATCTG	217
Db	2790860	TACGAATACGATCTTAAAGGCTATGTGTACATTCACAAATGGAAATTTGGGGCTGAGATCTG	2790919
QY	218	GGGAACCGGTCATAAAGCACTGTGATTTGACTCTTTTCCCTTGCAAAATGTTTTCCAGC	277
Db	2790920	GGGAACCGGTCATAAAGCACTGTGATTTGACTCTTTTCCCTTGCAAAATGTTTTCCAGC	2790979
QY	278	GGATGTTGATTTTGGGACCCCTTGCTGGCCGCAATTCAACAGTTGACGCTGCAAAAACCG	337
Db	2790980	GGATGTTGATTTTGGGACCCCTTGCTGGCCGCAATTCAACAGTTGACGCTGCAAAAACCG	2791039
QY	338	CACCTCGCCATTTGCCACTAGCCCGGATTAATCTCACTGACCAATAGTAAGGAGCCGGTG	397
Db	2791040	CACCTCGCCATTTGCCACTAGCCCGGATTAATCTCACTGACCAATAGTAAGGAGCCGGTG	2791099
QY	398	TGATGATTTTGGCTGGAGAAATTTGGCAATATTTTGCTTTCTTCAGATGACGTCAAAATAGTG	457
Db	2791100	TGATGATTTTGGCTGGAGAAATTTGGCAATATTTTGCTTTCTTCAGATGACGTCAAAATAGTG	2791159
QY	458	ACAACCAAGTACAAATTTGAGAGATGACCTTGCGTACGGTTTGTACTACAGCAGCTGG	517
Db	2791160	ACAACCAAGTACAAATTTGAGAGATGACCTTGCGTACGGTTTGTACTACAGCAGCTGG	2791219
QY	518	ATATCAGTTGGAATACGATCAACCTTCAACCAACATGGGTGTGAGAGAAAGATCCGG	577
Db	2791220	ATATCAGTTGGAATACGATCAACCTTCAACCAACATGGGTGTGAGAGAAAGATCCGG	2791279
QY	578	TCAACGCTTTCATGTTGTAGGCAAGTTGACACCAACTTCTCAAACTGTCTGAGGTTG	637
Db	2791280	TCAACGCTTTCATGTTGTAGGCAAGTTGACACCAACTTCTCAAACTGTCTGAGGTTG	2791339
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QY	698	TGAGACAGTTGGACAAATCCCGCTGCTATAGTTTCCCTTGTTGGGCTGTGAGCTGGG	757
Db	2791400	TGAGACAGTTGGACAAATCCCGCTGCTATAGTTTCCCTTGTTGGGCTGTGAGCTGGG	2791459
QY	758	CAATGATGGGTGTGCTGTGTGCTGTGCTGTGGGTGGATGGCAGGTTTCCCTAATTG	817
Db	2791460	CAATGATGGGTGTGCTGTGTGCTGTGCTGTGGGTGGATGGCAGGTTTCCCTAATTG	2791519
QY	818	CTTTTATTAACGCGCTTACAGATCATTTGCCAGACGTCATTTTGGGAAAAGAGGCTTGC	877
Db	2791520	CTTTTATTAACGCGCTTACAGATCATTTGCCAGACGTCATTTTGGGAAAAGAGGCTTGC	2791579

QY	87	CTACTTCTCTCCAAAATGTTGTGGAGTTTAAATGGCAACGCTGGCTGCATCGATTGCTT	937
Db	2791580	CTACTTCTCTCCAAAATGTTGTGGAGTTTAAATGGCAACGCTGGCTGCATCGATTGCTT	2791635
QY	938	ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAAACGAGCCAGATCAATCGATCTGGAA	997
Db	2791640	ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAAACGAGCCAGATCAATCGATCTGGAA	2791695
QY	998	TTGTTGTGCTGTTTGGCAGGTTTGACACATCTGTGCATCTCTGACGAGACGACATCACGGGCG	1057
Db	2791700	TTGTTGTGCTGTTTGGCAGGTTTGAACAATCTGTGCATCTCTGACGAGACGACATCACGGGCG	2791758
QY	1058	CTCCGGTGCACACAAAGTGACAGATTTTTCGAAACAATCTGTGTTAACGGGCGGCAATGTTG	1117
Db	2791760	CTCCGGTGCACACAAAGTGACAGATTTTTCGAAACAATCTGTGTTAACGGGCGGCAATGTTG	2791819
QY	1118	CTGCGGTGGGTTTGGGCATTAAGCTTTCTGAATATCTGCATGTCATGTTGTGCTGCATG	1177
Db	2791820	CTGCGGTGGGTTTGGGCATTAAGCTTTCTGAATATCTGCATGTCATGTTGTGCTGCATG	2791879
QY	1118	AGTCGGCTGCAGACCTTAATTAATTCGTCTAATTTGGCCCGCATTAATCGTGTGGCGTCA	1237
Db	2791880	AGTCGGCTGCAGACCTTAATTAATTCGTCTAATTTGGCCCGCATTAATCGTGTGGCGTCA	2791939
QY	1238	CCGACGCGGCTTCCAGATGGGTTGTATACGGGAGTGTCTCGGTGATTAATGCGGGGC	1297
Db	2791940	CCGACGCGGCTTCCAGATGGGTTGTATACGGGAGTGTCTCGGTGATTAATGCGGGGC	2791999
QY	1298	TTACTGCGCTGATGGGTTCTGCGTTTATTAATCTCTTCTGTTGTTATTAGAGCCCGCTT	1357
Db	2792000	TTACTGCGCTGATGGGTTCTGCGTTTATTAATCTCTTCTGTTGTTATTAGAGCCCGCTT	2792059
QY	1358	CTGCGCGCTGCAGTTCCTGCAACAGACAGATGGTTTACATGAGGTTTGGCTGGCCGTGAT	1417
Db	2792060	CTGCGCGCTGCAGTTCCTGCAACAGACAGATGGTTTACATGAGGTTTGGCTGGCCGTGAT	2792119
QY	1418	TCTTGATTCCACCGTTGATTTGGCGATGGCCGGATCACAACATGCTTCCAGAGTCTAG	1477
Db	2792120	TCTTGATTCCACCGTTGATTTGGCGATGGCCGGATCACAACATGCTTCCAGAGTCTAG	2792179
QY	1478	CAATTTCACGGGGAATGAGCCCAACCCGTGAATGATCAACATCTATGGGTTTACCCACA	1537
Db	2792180	CAATTTCACGGGGAATGAGCCCAACCCGTGAATGATCAACATCTATGGGTTTACCCACA	2792239
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Db	2792240	TTGCGGTTGCTTAAAGCCATCTGCTTATCACTTGGCGGTGGGCTGTTGGGTAGTGA	2792299
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QY	1658	ATGAGTTCTCTTCCAGAGGAGCTGAGCAAGATCAAGCGCGGCGACAGAAACGTCCAA	1717
Db	2792360	ATGAGTTCTCTTCCAGAGGAGCTGAGCAAGATCAAGCGCGGCGACAGAAACGTCCAA	2792419
QY	1718	AGACTAATCAGAGATTGGTAAATAAAGTAAATCAACCTGTGTTAGGGCTCTTTCGCT	1777
Db	2792420	AGACTAATCAGAGATTGGTAAATAAAGTAAATCAACCTGTGTTAGGGCTCTTTCGCT	2792479
QY	1778	TAAATAGGTAATGAGATTCGGGTGATGCTTTTAAACATCAGAGAGATCTCTTCCGGGCC	1837
Db	2792480	TAAATAGGTAATGAGATTCGGGTGATGCTTTTAAACATCAGAGAGATCTCTTCCGGGCC	2792539
QY	1838	AAAATCAACGACACTGTGCCACCCCGAATTCCTTACGCTGTGTAAGAGAGAAACGCA	1897
Db	2792540	AAAATCAACGACACTGTGCCACCCCGAATTCCTTACGCTGTGTAAGAGAGAAACGCA	2792599
QY	1898	GCGGCGG 1904	
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 Db 816 TGAACGAGTTGAGCAATCCCGCTGCTTATGATTTCCCTGTTGCGTTGCTGCTGAGG 875  
 QY 758 CAATGATGAGTGTGCTGTTGCTGCTGTTGAGTGTGATGAGTGTGATGAGTGTGATG 817  
 Db 876 CAATGATGAGTGTGCTGTTGCTGCTGTTGAGTGTGATGAGTGTGATGAGTGTGATG 935  
 QY 818 CTTTATTTACCGGCTTACCATCATTTGCGACAGATGTTTGGGAAAAGAGGTTTGC 877  
 Db 936 CTTTATTTACCGGCTTACCATCATTTGCGACAGATGTTTGGGAAAAGAGGTTTGC 995  
 QY 878 CTACTTTCTTCAAAATGTTGTTGTTGTTTATGCGACGCTGCTGATCATGATTCCT 937  
 Db 996 CTACTTTCTTCAAAATGTTGTTGTTTATGCGACGCTGCTGATCATGATTCCT 1055  
 QY 938 ATTCTTTGGCGTTGCAATTTGCTTGAATCAAAACGAGCCAGATCATGCTGAGAA 997  
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 QY 998 TTTGTTGCTGTTGAGGAGTTTGAACCTGCGCAATCTGCGAGAGCGGATCAACGGCG 1057  
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 QY 1238 CCGGAGCGGCTTCCGAGTGTGTTACGCGAGTGTCTCGGTGATTTATGCGGAGG 1297  
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 Db 1476 CTGCGCTGCGATTTGCTGCAACAGAGTGTGTTGCTGCTGCTGCTGCTGCTG 1535  
 QY 1418 TCTTGATTTCAACGTTGATTTGCGGATTTGCGGATTCACACCAATGCTTCAAG 1477  
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 QY 1478 CAATTTACCGGGAATGTAACGCACTTGAATGATCAAACTGATGAGTTTCAAC 1537  
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 QY 1538 TTTGCGGTTGCTTTAGCACTGCTTCACTGCGCTGCGTGGTTTGGTGTGATG 1597  
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 Db 1896 TAAATAGCTGATGAATATCGGCTGATGCTTTTAAACATCAGAGAGATCCTGCGG 1955  
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 Db 1956 AATAATCAGAGACTGCTCCACCCAGAAATCCCTGACGCTGTGGAAGAGAAACCGCA 2015  
 QY 1898 GCCGGGG 1904  
 Db 2016 GCCGGTG 2022

RESULT 9  
 US-09-963-521-1  
 : Sequence 1, Application US/09963521  
 : Patent No. US20020146781A1  
 : GENERAL INFORMATION:  
 : APPLICANT: ZIEGLER, PETRA  
 : APPLICANT: EISELING, LOTHAR  
 : APPLICANT: SAHM, HERMANN  
 : TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE  
 : TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF  
 : TITLE OF INVENTION: L-THREONINE USING CORYNEFORM BACTERIA  
 : FILE REFERENCE: 21123/282413/MAS  
 : CURRENT APPLICATION NUMBER: US/09/963,521  
 : PRIOR FILING DATE: 2001-09-27  
 : PRIOR APPLICATION NUMBER: 09/431,099  
 : PRIOR FILING DATE: 1999-11-01  
 : PRIOR APPLICATION NUMBER: DE 199 41 478.5  
 : NUMBER OF SEQ ID NOS: 10  
 : SOFTWARE: PatentIn Ver. 2.1  
 : SEQ ID NO 1  
 : LENGTH: 2817  
 : TYPE: DNA  
 : ORGANISM: Corynebacterium glutamicum  
 : FEATURE:  
 : NAME/KEY: CDS  
 : LOCATION: (398)..(1864)  
 : OTHER INFORMATION: three-Gen  
 : US-09-963-521-1

Query Match 96.2%; Score 1836.6; DB 9; Length 2817;  
 Best Local Similarity 99.0%; Pred. No. 0;  
 Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 38 CCCCCTTACCTGATGTTATGAGCTGAGAGAGACTTGAACCTCTCAACCTAGACATTA 97  
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 QY 158 TACGAATACGATCTTAAAGGATGATGATCATCAATGGAATTCGGGGCTAGATATC 217  
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 QY 278 GGAATGATGATTTTGGAGACCTTCTGCTGCGCATTTTCAACATTTACCGTGAAGAGCG 337  
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 QY 338 CACCTCCGCAATGCGACATGAGCCCGGATGATGATCTACTGACCAATGATCAAGTGGCGG 397  
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QY 398 TGAATTTGGCTGCGGAAATTTGGCAATTTTCTTCAAGTAAGTCAAAATAGT 457  
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Db 576 ATACCAAGTTCAGAGTTGAGCAGTCTGCGGTGAGTTGTAACACAGCAGTGG 635  
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QY 518 ATATCAGTTGAATACAGTACATCTTCAACCAATCGGTGAGAGAGAGATGCGG 577  
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Db 636 ATATCAGTTGAATACAGTACATCTTCAACCAATCGGTGAGAGAGAGATGCGG 695  
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QY 578 TCAACGTTTCAATGTTGTAAGCAAGTTGACACCAACTTCTCAAACTGTCTGAGTTG 637  
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QY 698 TGAAGAGTTGAGCAATCCCTGCGTCTTATGTTTCCGTTGCGTTGCTGGTGG 757  
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QY 1238 CCGAGCGGCTTTCGAGTGGTGTGTAACGCGAGTGTCTCGATGATTAATGCGGCG 1297  
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Db 1356 CCGAGCGGCTTTCGAGTGGTGTGTAACGCGAGTGTCTCGATGATTAATGCGGCG 1415  
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QY 1298 TTACGCGGTGATGGGTTGCTGCTTATTAATCTCTGTTGTTTATTTAGGCGCGTCT 1357  
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Db 1416 TTACGCGGTGATGGGTTGCTGCTTATTAATCTCTGTTGTTTATTTAGGCGCGTCT 1475  
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QY 1358 CTGCGGTGCGATGCTGCAAGAGTGTGTTCACTGAGTGTGCTGCGCGCAT 1417  
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Db 1476 CTGCGGTGCGATGCTGCAAGAGTGTGTTCACTGAGTGTGCTGCGCGCAT 1535  
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QY 1478 CAATTTACCGGGAATGAGTACGCCACCTGATGATCAAAACATCATGAGTTTCAACA 1537  
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QY 1598 TTGCGCGGAGGCTTACGCTGCTTCAACAGCCTTCAACCAATACCTGATTTTCAAGCGGA 1657  
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Db 1836 AGACTAATCAAGATTCGTTAATTAAGTAAATCAACTGCTTGAAGCGCTCTTGGCT 1895  
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Db 1896 TAAATGCGTAATATGCGGTGATGCTTTTAAACATCAGAGGATCTTGGCGGCC 1955  
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QY 1838 AAATCAAGCACTGCTCCACCCAGAAATCCCTGACGCTGTGAAGAGAAACCGCA 1897  
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QY 1898 GCCGCGG 1904  
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Db 2016 GCCGCGG 2022  
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RESULT 10  
US-09-834-721-1  
; Sequence 1, Application US/09834721  
; Patent No. US2002015551A1  
; GENERAL INFORMATION:  
; APPLICANT: RIEBING, MECHTILD  
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE  
; FILE REFERENCE: 21133/280169/WAS  
; CURRENT APPLICATION NUMBER: US/09/834,721  
; CURRENT FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: DE 100 26 494.8  
; PRIOR FILING DATE: 2000-05-27  
; PRIOR APPLICATION NUMBER: DE 101 02 823.7  
; PRIOR FILING DATE: 2001-01-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2817  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
; FEATURE:  
; OTHER INFORMATION: ATCC14752  
; NAME/KEY: CDS  
; LOCATION: (398)..(1864)  
; OTHER INFORMATION: three gene  
US-09-834-721-1  
Query Match 96.2%; Score 1836.6; DB 9; Length 2817;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
QY 38 CCCCTTTGACCTGGGTGTTATTTGAGCTGAGAAAGAACTTGAACCTCAACGATTA 97  
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Db 156 CCCCTTTGACCTGGGTGTTATTTGAGCTGAGAAAGAACTTGAACCTCAACGATTA 215  
| | | | |  
QY 98 CAAGTGGCTTGGCGCAATGGCCCACTCCAGCAACCGCAAGTGGTGAATCAACAAC 157  
| | | | |  
Db 216 CAAGTGGCTTGGCGCAATGGCCCACTCCAGCAACCGCAAGTGGTGAATCAACAAC 275  
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QY 158 TAGGAATGATCTTTAGCGTATGTGTAATCAACAATGGAATTGCGGCGCTAGAGTATCTG 217  
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Query Match		96.2%;	Score 1836.6;	DB 9;	Length 2817;
Best Local Similarity		99.0%;	Pred. No. 0;		
Matches 1848;		Conservative 0;	Mismatches 19;	Indels 0;	Gaps 0;
QY	38	CCCCCTTGACCTGGTGTATTTAGCTGAGAGAGACTTGAACCTCTCAACCTACGCACTTA	97		
DB	156	CCCCCTTGACCTGGTGTATTTAGCTGAGAGAGACTTGAACCTCTCAACCTACGCACTTA	215		
QY	98	CAAGTGGCTTGGCTGCGCAATTGGCGCACTTCAGCAGCCGAGATGTGATGATCAACAC	157		
DB	216	CAAGTGGCTTGGCTGCGCAATTGGCGCACTTCAGCAGCCGAGATGTGATGATCAACAC	275		
QY	158	TACGAATACGATCTTATGCGTATGTATGATCAATGAAATTCGGGGCTTATGATCTG	217		
DB	276	TACGAATACGATCTTATGCGTATGTATGATCAATGAAATTCGGGGCTTATGATCTG	335		
QY	218	GTGAACCGTGCATTAAGACCTGTGATTTGACTCTTTCTTTCGCAAAATGTTTCCAGC	277		
DB	336	GTGAACCGTGCATTAAGACCTGTGATTTGACTCTTTCTTTCGCAAAATGTTTCCAGC	395		
QY	278	GGATGTTGAGTTTGGGACCTTGTGGCGCATTTCAACAGTTGACGCTGCAAAAGCCG	337		
DB	396	GGATGTTGAGTTTGGGACCTTGTGGCGCATTTCAACAGTTGACGCTGCAAAAGCCG	455		
QY	338	CACCTCGGCAATGGCACTAGCCCGCATTTGATCTCACTGACCAATGTAAGTGCGCGTG	397		
DB	456	CACCTCGGCAATGGCACTAGCCCGCATTTGATCTCACTGACCAATGTAAGTGCGCGTG	515		
QY	398	TGATGAATTTGGCTGGAGAAATGGCGAATTTTGGCTTTCTTCAAGTTACGTCGAATAGTG	457		
DB	516	TGATGAATTTGGCTGGAGAAATGGCGAATTTTGGCTTTCTTCAAGTTACGTCGAATAGTG	575		
QY	458	ACACCAAGTTCAAGTTTCAGCACTGTAACCTTGCCTGATCGGTTTGTATCTACACGACAGTG	517		
DB	576	ATACCAAGTTCAAGTTTCAGCACTGTAACCTTGCCTGATCGGTTTGTATCTACACGACAGTG	635		
QY	518	ATATCAGTTGAATAGATTCACATCTTACCAACATCGGTGGAGAGAGAAATGCCG	577		
DB	636	ATATCAGTTGAATAGATTCACATCTTACCAACATCGGTGGAGAGAGAAATGCCG	695		
QY	578	TCACCGTGTTCATGTTGTAGGCAATGGGCAACCAACTTCTCAAACTGTCTGAGGTTG	637		
DB	696	TCACCGTGTTCATGTTGTAGGCAATGGGCAACCAACTTCTCAAACTGTCTGAGGTTG	755		
QY	638	ACCGTTGATCCGTTCAATTAGGCTGGTGGCAACCCGCTGAGGTTGCCGAGAAATCC	697		
DB	756	ACCGTTGATCCGTTCAATTAGGCTGGTGGCAACCCGCTGAGGTTGCCGAGAAATCC	815		
QY	698	TGACGAGTTGAGCAATCCCTGCGGTCTTATGTTTCCCTGTTGGCTTGGCTGGG	757		
DB	816	TGACGAGTTGAGCAATCCCTGCGGTCTTATGTTTCCCTGTTGGCTTGGCTGGG	875		
QY	758	CAATGATGGGTGGTGTGCTGTGCTGTGCTGGTGGGATGAGAGGTTTCCCTAATTG	817		
DB	876	CAATGATGGGTGGTGTGCTGTGCTGTGCTGGTGGGATGAGAGGTTTCCCTAATTG	935		
QY	818	CTTTTATTAACCGGCTTCAGATCATTTGCCAGACGTCATTTTGGGAAAGAGGTTTGC	877		
DB	936	CTTTTATTAACCGGCTTCAGATCATTTGCCAGACGTCATTTTGGGAAAGAGGTTTGC	995		
QY	878	CTACTTCTTCCAAATGTTGTGGTGTATTTAGCCAGCGTGCCTGATGATGTTGCT	937		
DB	996	CTACTTCTTCCAAATGTTGTGGTGTATTTAGCCAGCGTGCCTGATGATGTTGCT	1055		
QY	938	ATTCTTTGGCGTTGCAATTTGGTCTTGAATCAAAACCGAGCCAGATCATCGATCTGGA	997		
DB	1056	ATTCTTTGGCGTTGCAATTTGGTCTTGAATCAAAACCGAGCCAGATCATCGATCTGGA	1115		
QY	998	TTGTTGGCTGTTGGCAAGTTTGAACATCTGTCATCTTGTGAGAGACGGATCACGGCG	1057		
DB	1116	TTGTTGGCTGTTGGCAAGTTTGAACATCTGTCATCTTGTGAGAGACGGATCACGGCG	1175		
QY	1058	CTCCGGTACAGCAAGTGCACAGATTTTGAACACTCTGTTACCGCGGCAATTGTTG	1117		

DB	1176	CTCCGGTACAGAGAGTGCACGATTTTGTAAACACTCTGTTTACCGGGGCAATTTTG	1235		
QY	1118	CTGGCGTGGGTTTGGGATTCAGCTTCTGAAATCTTGCAATGTATGATTTGCTGCCATGG	1177		
DB	1236	CTGGCGTGGGTTTGGGATTCAGCTTCTGAAATCTTGCAATGTATGATTTGCTGCCATGG	1295		
QY	1178	AGTCCGCTGAGACACCTTAATTATGCTCAATTTGCGCGGATTAATGCTGGTGGCGTCA	1237		
DB	1296	AGTCCGCTGAGACACCTTAATTATGCTCAATTTGCGCGGATTAATGCTGGTGGCGTCA	1355		
QY	1238	CCGAGCGGCTTTGCAAGTGGGTTGTAACGCGAGTGGTCTCGGTATTAATTCGGGGCG	1297		
DB	1356	CCGAGCGGCTTTGCAAGTGGGTTGTAACGCGAGTGGTCTCGGTATTAATTCGGGGCG	1415		
QY	1298	TTACTGGCTGATGAGGTTCTGCGTTTATTAACCTCTTCTGTTTATTAAGCCCGTCT	1357		
DB	1416	TTACTGGCTGATGAGGTTCTGCGTTTATTAACCTCTTCTGTTTATTAAGCCCGTCT	1475		
QY	1358	CTGCCGCTGATGCTGCAACAGAGTGGTTTCACTGGTGGTTGCTTCCCGTGCAT	1417		
DB	1476	CTGCCGCTGATGCTGCAACAGAGTGGTTTCACTGGTGGTTGCTTCCCGTGCAT	1535		
QY	1418	TCTTGAATCCAGCTTGAATTTGGCGATTTGCCGCAATCAACCAATGCTTCCAGTCTAG	1477		
DB	1536	TCTTGAATCCAGCTTGAATTTGGCGATTTGCCGCAATCAACCAATGCTTCCAGTCTAG	1595		
QY	1478	CAATTTACCGCGGAATGTAGCCACCTGATATTAACACTCATGAGGTTTCAACACCA	1537		
DB	1596	CAATTTACCGCGGAATGTAGCCACCTGATATTAACACTCATGAGGTTTCAACACCA	1655		
QY	1538	TTGCGGTTCTTTAGGCACTGCTTCATCACTTGCCTGGCGGTGTTGGGTGAGTGA	1597		
DB	1656	TTGCGGTTCTTTAGGCACTGCTTCATCACTTGCCTGGCGGTGTTGGGTGAGTGA	1715		
QY	1598	TTGCCGAGGCTACGCTGCTTCAACAGCTTCAACCCATACCTGATTTACCAAGCGCA	1657		
DB	1716	TTGCCGAGGCTACGCTGCTTCAACAGCTTCAACCCATACCTGATTTACCAAGCGCA	1775		
QY	1658	ATGAGTTCCTTCCAGAGGAAAGCTGACGACGATATAGCGCGGCGAGAAAGCTGCCA	1717		
DB	1776	ATGAGTTCCTTCCAGAGGAAAGCTGACGACGATATAGCGCGGCGAGAAAGCTGCCA	1835		
QY	1718	AGACTAATCAGAGATTCGCTTAATTAAGGTAAATCAACTGCTTAGCGCTTTCGCT	1777		
DB	1836	AGACTAATCAGAGATTCGCTTAATTAAGGTAAATCAACTGCTTAGCGCTTTCGCT	1895		
QY	1778	TAAATAGCGTGAATATCGGCTGATGCTTTTAAACACTCAGAGAGATCCTTGCAGCC	1837		
DB	1896	TAAATAGCGTGAATATCGGCTGATGCTTTTAAACACTCAGAGAGATCCTTGCAGCC	1955		
QY	1838	AAATCAGGAGCACTGCTCCCAACCCAGAAATCCCTTCAAGCTGTTGAAGAGAAACCGCA	1897		
DB	1956	AAATCAGGAGCACTGCTCCCAACCCAGAAATCCCTTCAAGCTGTTGAAGAGAAACCGCA	2015		
QY	1898	GCCGGGG 1904			
DB	2016	GCCGGTG 2022			

RESULT 12  
 US-09-951-535-1  
 ; Sequence 1, Application US/09951535  
 ; Publication No. US2003049802A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ZIEGLER, PETRA  
 ; APPLICANT: EGBELING, LOTMAR  
 ; APPLICANT: SAHM, HERMANN  
 ; APPLICANT: THIERBACH, GEORG  
 ; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND  
 ; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE  
 ; FILE REFERENCE: 21123/282415/MAS





QY 1718 AGACTATCAGAGATTGGTAAATAAAGGTAAATCAACCTGCTTGGCTTTCGCT 1777  
 DB 1836 AGACTATCAAGATTGGTAAATAAAGGTAAATCAACCTGCTTGGCTTTCGCT 1895  
 QY 1778 TAAATGCGTAGAATTCGGGTCGATCGCTTTAAACACTCAGAGGATCTTGGCGGC 1837  
 DB 1896 TAAATGCGTAGAATTCGGGTCGATCGCTTTAAACACTCAGAGGATCTTGGCGGC 1955  
 QY 1838 AAAATCAGGACGACGTCGCCACCCGAGAAATCCCTTCAGCGTGTGAAGAGAACCGCA 1897  
 DB 1956 AAAATCAGGACGACGTCGCCACCCGAGAAATCCCTTCAGCGTGTGAAGAGAACCGCA 2015  
 QY 1898 GCCGCGG 1904  
 DB 2016 GCCGCGG 2022

RESULT 14  
 US-10-627-476-557  
 ; Sequence 557, Application US/10627476  
 ; Publication No. US2004030116A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pompejus, Mark  
 ; APPLICANT: Kroege, Burkhard  
 ; APPLICANT: Schoder, Hartwig  
 ; APPLICANT: Zeider, Oskar  
 ; APPLICANT: Heberhauser, Gregor  
 ; TITLE OF INVENTION: CORVNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
 ; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
 ; FILE REFERENCE: BGI-125CPN  
 ; CURRENT APPLICATION NUMBER: US/10/627,476  
 ; PRIOR FILING DATE: 2003-07-25  
 ; PRIOR APPLICATION NUMBER: 09/602,787  
 ; PRIOR FILING DATE: 2000-06-23  
 ; PRIOR APPLICATION NUMBER: USSN 60/141031  
 ; PRIOR FILING DATE: 1999-06-25  
 ; PRIOR APPLICATION NUMBER: DE 19931454.3  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: DE 19931478.0  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: DE 19931563.9  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: DE 19932122.1  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932124.8  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932125.6  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932128.0  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932180.9  
 ; PRIOR FILING DATE: 1999-07-09  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 678  
 ; SEQ ID NO 557  
 ; LENGTH: 1530  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium glutamicum  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (101)..(1567)  
 ; OTHER INFORMATION: RXN00349  
 ; US-10-627-476-557

Query Match 83.3%; Score 1590; DB 13; Length 1590;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 TGTGTACATCAGATGATTCGGGCTTAGAGTATCTGTGAACGCTGATTAAGACCT 239  
 DB 1 TGTGTACATCAGATGATTCGGGCTTAGAGTATCTGTGAACGCTGATTAAGACCT 60

QY 240 GTGATTGACCTCTTTTCTTGGAAAAATGTTTCCAGCGAGATGTGATTTTCCGCCCT 299  
 DB 61 GTGATTGACCTCTTTTCTTGGAAAAATGTTTCCAGCGAGATGTGATTTTCCGCCCT 120  
 QY 300 TGTGCGCGCATTTTCAACAGTTGAGCGCTGCAAAAGCCGACCTCCGCCATCGCATACG 359  
 DB 121 TGTGCGCGCATTTTCAACAGTTGAGCGCTGCAAAAGCCGACCTCCGCCATCGCATACG 180  
 QY 360 CCCGATGATTCACACGACATGATGATGATGATGATGATGATGATGATGATGATGAT 419  
 DB 181 CCCGATGATTCACACGACATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
 QY 420 TGGCGATATTTGCTTCTTCAAGTACGTACAAATAGTACACCAAGTACAAAGTTGAGC 479  
 DB 241 TGGCGATATTTGCTTCTTCAAGTACGTACAAATAGTACACCAAGTACAAAGTTGAGC 300  
 QY 480 AGTACCTTGGCGAGGTTTGTACTACACGACGTGAGATATACCTGATACGATCAC 539  
 DB 301 AGTACCTTGGCGAGGTTTGTACTACACGACGTGAGATATACCTGATACGATCAC 360  
 QY 540 CATCTTCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 599  
 DB 361 CATCTTCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
 QY 600 CAAGTTGACACCAACTTCTCAAACTGCTGAGGTTGACCGTTGATCCGTTCAATCA 639  
 DB 421 CAAGTTGACACCAACTTCTCAAACTGCTGAGGTTGACCGTTGATCCGTTCAATCA 480  
 QY 660 GGTGTGCGACCCCGCTGAGTTGGCGAGAAATCTGAGACGATGAGACGATGAGCC 719  
 DB 481 GGTGTGCGACCCCGCTGAGTTGGCGAGAAATCTGAGACGATGAGACGATGAGCC 540  
 QY 720 TGGCTTATGATTTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 779  
 DB 541 TGGCTTATGATTTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
 QY 780 TGTGCTGTGGGTGGTGGATGAGAGTTTCCCTAATGCTTTATTAACCGGTTCAAGAT 839  
 DB 601 TGTGCTGTGGGTGGTGGATGAGAGTTTCCCTAATGCTTTATTAACCGGTTCAAGAT 660  
 QY 840 CATTGCCACGACGCTATTTTGGGAAAGGTTGGCTTCTTCCAAAATGTTGT 899  
 DB 661 CATTGCCACGACGCTATTTTGGGAAAGGTTGGCTTCTTCCAAAATGTTGT 720  
 QY 900 TGTGCTTTTATTCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 959  
 DB 721 TGTGCTTTTATTCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
 QY 960 TCTTGATCAAAACGAGCCAGATCATGCAATGGAATGTTGTGCTGTTGGCAGGTTT 1019  
 DB 781 TCTTGATCAAAACGAGCCAGATCATGCAATGGAATGTTGTGCTGTTGGCAGGTTT 840  
 QY 1020 GACACTGCTGCAATCTGCGAGGAGGATCAGCGGCGCTCGGCTGAGACGAGTGCACG 1079  
 DB 841 GACACTGCTGCAATCTGCGAGGAGGATCAGCGGCGCTCGGCTGAGACGAGTGCACG 900  
 QY 1080 ATTTTGAACACACTCTGTTTACCGGCGGCAATGTTGCTGCGGTTTGGGATTTCA 1139  
 DB 901 ATTTTGAACACACTCTGTTTACCGGCGGCAATGTTGCTGCGGTTTGGGATTTCA 960  
 QY 1140 GCTTCTGAATCTTGCATGTCATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1199  
 DB 961 GCTTCTGAATCTTGCATGTCATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 QY 1200 TTTGCTTACATTCGCGCGCATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1259  
 DB 1021 TTTGCTTACATTCGCGCGCATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
 QY 1260 TTTGCTTACGCGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1319  
 DB 1081 TTTGCTTACGCGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 QY 1320 GTTTTATTAACCTTCTGTTGTTTATTTAGGCCCGCTGCTGCGCGTGCATGTTGCAAC 1379

Db 1141 GTTTATTACCTCTTCGTTGTTTATTAGAGCCCGCTCTGCGCGTGCGATTGCTGCAAC 1200  
QY 1380 AGCAGTTGGTTTCACTGGTGGTTTGCTTGGCCGTCGATTCCTTGATTCACCGTATGTTG 1439  
Db 1201 AGCAGTTGGTTTCACTGGTGGTTTGCTTGGCCGTCGATTCCTTGATTCACCGTATGTTG 1260  
QY 1440 GGGCATTGGCCGGGATTCACCAATGCTTCCAGTCTTGAGCAATTTTACCGCGAATGTAAGC 1499  
Db 1261 GGGCATTGGCCGGGATTCACCAATGCTTCCAGTCTTGAGCAATTTTACCGCGAATGTAAGC 1320  
QY 1500 CACCTGATGATTAACCACTCATGGGTTTCCAAACATTTGGGTTGCTTTAGCCATGTC 1559  
Db 1321 CACCTGATGATTAACCACTCATGGGTTTCCAAACATTTGGGTTGCTTTAGCCATGTC 1380  
QY 1560 TTTCATCACTTGGCGCTGGCGTGGTTTGGGTGATGATGATGCGCAGGCTACGTCGTC 1619  
Db 1381 TTTCATCACTTGGCGCTGGCGTGGTTTGGGTGATGATGATGCGCAGGCTACGTCGTC 1440  
QY 1620 ACCACGCTTCAACCCATACCGTGCATTTTACCAAGCGCAATGATGTTCTTCCAGAGGA 1679  
Db 1441 ACCACGCTTCAACCCATACCGTGCATTTTACCAAGCGCAATGATGTTCTTCCAGAGGA 1500  
QY 1680 AGCTGAGCAGATCAGCGCGCGCAGAGAAACGTCGAAGACTAATGAGATTCCGTTAA 1739  
Db 1501 AGCTGAGCAGATCAGCGCGCGCAGAGAAACGTCGAAGACTAATGAGATTCCGTTAA 1560  
QY 1740 TAAAGGTAAATCAACCTGCTTAGGCGT 1769  
Db 1561 TAAAGGTAAATCAACCTGCTTAGGCGT 1590

## RESULT 15

US-10-450-055-41  
; Sequence 41, Application US/10450055  
; Publication No. US20040043953A1  
; GENERAL INFORMATION:  
; APPLICANT: BASF Aktiengesellschaft  
; TITLE OF INVENTION: No. US20040043953A1 genes of *Corynebacterium*  
; FILE REFERENCE: 936, 2000  
; CURRENT APPLICATION NUMBER: US/10/450,055  
; CURRENT FILING DATE: 2003-06-10  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Vers. 2.0  
; SEQ ID NO 41  
; LENGTH: 1590  
; TYPE: DNA  
; ORGANISM: *Corynebacterium glutamicum*  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (101)..(1567)  
; OTHER INFORMATION: RKS00349  
US-10-450-055-41

Query Match 83.3%; Score 1590; DB 13; Length 1590;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 TGTGTACATCAATGGAATTCGCGGCTAGAGTATCTGTGAACGTCATTAACGACCT 239  
Db 1 TGTGTACATCAATGGAATTCGCGGCTAGAGTATCTGTGAACGTCATTAACGACCT 60  
QY 240 GTGATTTGACCTCTTTTCTTGGCAAAATGTTTCCAGCGGATGTTGAGTTTGCACCT 299  
Db 61 GTGATTTGACCTCTTTTCTTGGCAAAATGTTTCCAGCGGATGTTGAGTTTGCACCT 120  
QY 300 TGTGAGCGCATTTTCAACAGTTGACGCTGCAAAAGCGGACCTCGGCACTGGCACTAGC 359  
Db 121 TGTGAGCGCATTTTCAACAGTTGACGCTGCAAAAGCGGACCTCGGCACTGGCACTAGC 180  
QY 360 CCGGATGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAT 419  
Db 181 CCGGATGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAT 240

QY 420 TGGGATATTTTGGTTTCTTCAAGTACGTCAAAATAGTACCAAGGATACAGTTGAGC 479  
Db 241 TGGGATATTTTGGTTTCTTCAAGTACGTCAAAATAGTACCAAGGATACAGTTGAGC 300  
QY 480 AGTACCTTGGCGTACGGTTTGTACTACAGCAAGTGGATATGACGTTGAATAGATCAC 539  
Db 301 AGTACCTTGGCGTACGGTTTGTACTACAGCAAGTGGATATGACGTTGAATAGATCAC 360  
QY 540 CATTTTACCAACATCGGTGTGAGAGGAAAGATGCCGTCAACGTTTCAATGTTGAG 599  
Db 361 CATTTTACCAACATCGGTGTGAGAGGAAAGATGCCGTCAACGTTTCAATGTTGAG 420  
QY 600 CAAGTTGACACCAACCTTCCAACTGTCGAGTTGACCGTTTGAATCCGTTCAATCA 659  
Db 421 CAAGTTGACACCAACCTTCCAACTGTCGAGTTGACCGTTTGAATCCGTTCAATCA 480  
QY 660 GGTGTGTGCGACCCCGCTGAGGTTGGCGAAGAAATCTGAGCAGATTGAGCAATCCC 719  
Db 481 GGTGTGTGCGACCCCGCTGAGGTTGGCGAAGAAATCTGAGCAGATTGAGCAATCCC 540  
QY 720 TGGTCTTAATGTTTCCCTTGGCTTGGCTTGGCTGGGCAATGATGGGTGGTCTGTTGC 779  
Db 541 TGGTCTTAATGTTTCCCTTGGCTTGGCTTGGCTGGGCAATGATGGGTGGTCTGTTGC 600  
QY 780 TGTGCTGTGGGTGATGATGAGAGTTTCCCTAATGCTTTTATTAACGCGGTTCAAGAT 839  
Db 601 TGTGCTGTGGGTGATGATGAGAGTTTCCCTAATGCTTTTATTAACGCGGTTCAAGAT 660  
QY 840 CATTTGCAAGCAGCTCAATTTTGGGAAAGAAAGGTTTGGCTACTTCTTCCAAATGTTG 899  
Db 661 CATTTGCAAGCAGCTCAATTTTGGGAAAGAAAGGTTTGGCTACTTCTTCCAAATGTTG 720  
QY 900 TGGTGTGTTTATTTGCCACGCTGCTGCTGATGATGCTTATTTCTTTGGCGTTGCAATTTGG 959  
Db 721 TGGTGTGTTTATTTGCCACGCTGCTGCTGATGATGCTTATTTCTTTGGCGTTGCAATTTGG 780  
QY 960 TCTTGAGATCAAAACGAGCCAGATCATGCAATCGAATGTTGTGCTGTGTCAGGTT 1019  
Db 781 TCTTGAGATCAAAACGAGCCAGATCATGCAATCGAATGTTGTGCTGTGTCAGGTT 840  
QY 1020 GACACTGTGCAATCTTCCAGAGCGGATCAACGCGCGCTCCGCTGACAGCAATGTCAGC 1079  
Db 841 GACACTGTGCAATCTTCCAGAGCGGATCAACGCGCGCTCCGCTGACAGCAATGTCAGC 900  
QY 1080 ATTTTTCGAAACATCTCTGTTTACCGGCGGCAATGTTGCTGGGTGGGTTTGGCAATTC 1139  
Db 901 ATTTTTCGAAACATCTCTGTTTACCGGCGGCAATGTTGCTGGGTGGGTTTGGCAATTC 960  
QY 1140 GCTTCTGAAATCTTGATGATGATGCTGCTGCGATGAGTCCGCTGACAGCACTAATTA 1199  
Db 961 GCTTCTGAAATCTTGATGATGATGCTGCTGCGATGAGTCCGCTGACAGCACTAATTA 1020  
QY 1200 TTGCTCTACATTTGCGCGCATTAATGCTGTGAGGCTCAACGCGACGCGCTTGCAGTGG 1259  
Db 1021 TTGCTCTACATTTGCGCGCATTAATGCTGTGAGGCTCAACGCGACGCGCTTGCAGTGG 1080  
QY 1260 TTGTTACGCGAGTGTCTCTCGGTATTAATTCGCGGCTTACTGCGCTATGAGGTTCTGC 1319  
Db 1081 TTGTTACGCGAGTGTCTCTCGGTATTAATTCGCGGCTTACTGCGCTATGAGGTTCTGC 1140  
QY 1320 GTTTTATTAACCTCTTGTGTTTATTTAGGACCCGCTCTGCGCGCTGCAATGCTCAAC 1379  
Db 1141 GTTTTATTAACCTCTTGTGTTTATTTAGGACCCGCTCTGCGCGCTGCAATGCTCAAC 1200  
QY 1380 AGCAGTTGGTTTCACTGGTGGTTTGCTTGGCCGTCGATTCCTTGATTCACCGTATGTTG 1439  
Db 1201 AGCAGTTGGTTTCACTGGTGGTTTGCTTGGCCGTCGATTCCTTGATTCACCGTATGTTG 1260  
QY 1440 GGGCATTGGCCGGGATTCACCAATGCTTCCAGTCTTGAGCAATTTTACCGCGAATGTAAGC 1499  
Db 1261 GGGCATTGGCCGGGATTCACCAATGCTTCCAGTCTTGAGCAATTTTACCGCGAATGTAAGC 1320

QY 1500 CACCTGAATGATCAAAAGCTCATGGTTTCACCAACATTCGGGTGCTTTAGCACTGC 1559  
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 Db 1321 CACCTGAATGATCAAAAGCTCATGGTTTCACCAACATTCGGGTGCTTTAGCACTGC 1380  
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 QY 1560 TTGATCACTGCGCGTGGCGTGGTTTGGGTGAGTGGATTGCCCGAGGCTACGTGTC 1619  
 |||||  
 Db 1381 TTGATCACTGCGCGTGGCGTGGTTTGGGTGAGTGGATTGCCCGAGGCTACGTGTC 1440  
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 QY 1620 ACCACGCTTGAACCCATACCGTGCAATTACCAAGGCGAATGAGTTCTCTTCCAGAGGA 1679  
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 Db 1441 ACCACGCTTGAACCCATACCGTGCAATTACCAAGGCGAATGAGTTCTCTTCCAGAGGA 1500  
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 QY 1680 AGCTGAGCAAAATCAGGCGCGGAGAGAAAGTCCAAAGACTAATCAGAGATTGAGTAA 1739  
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 Db 1501 AGCTGAGCAAAATCAGGCGCGGAGAGAAAGTCCAAAGACTAATCAGAGATTGAGTAA 1560  
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 QY 1740 TAAAGGTAAATCAACTGCTTAGGCGT 1769  
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 Db 1561 TAAAGGTAAATCAACTGCTTAGGCGT 1590  
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Search completed: July 31, 2004, 10:01:38  
 Job time : 831.413 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 31, 2004, 09:27:29 ; Search time 1068 Seconds

(without alignments)  
143,624 Million cell updates/sec

Title: US-09-963-521-2

Perfect score: 2432  
Sequence: 1 MLSFATLRGRISTVDAKAA.....QNRGRKPKTNQRFNKR 489

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 segs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
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18: /cgn2\_6/ptodara/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2432	100.0	489	9	US-09-951-536-2
2	2432	100.0	489	9	US-09-951-536-4
3	2432	100.0	489	9	US-09-963-521-2
4	2432	100.0	489	9	US-09-963-521-4
5	2432	100.0	489	9	US-09-834-721-2
6	2432	100.0	489	9	US-09-834-721-4
7	2432	100.0	489	9	US-09-783-388-2
8	2432	100.0	489	9	US-09-783-388-4
9	2432	100.0	489	10	US-09-951-535-2
10	2432	100.0	489	10	US-09-951-535-4
11	2432	100.0	489	12	US-10-627-476-558
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19	134	5.5	376	9	US-09-738-626-6189	Sequence 6189, Ap
20	134	5.5	704	14	US-10-156-761-11225	Sequence 11225, A
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## ALIGNMENTS

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RESULT 1
US-09-951-536-2
; Sequence 2, Application US/09951536
; Patent No. US20020107378A1
; GENERAL INFORMATION:
; APPLICANT: ZIRGLER, PETRA
; APPLICANT: EGGELING, LOTMAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE TRP GENE AND
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
; TITLE OF INVENTION: USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282414/MAS
; CURRENT APPLICATION NUMBER: US/09/951,536
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-951-536-2

Query Match      100.0%; Score 2432; DB 9; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.56-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
US-09-951-536-4  
Sequence 4, Application US/09951536  
Patent No. US20020107378A1  
GENERAL INFORMATION:  
APPLICANT: ZIEGLER, PETRA  
APPLICANT: EGGELING, LOTMAR  
APPLICANT: SAHM, HERMANN  
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND  
TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE  
TITLE OF INVENTION: USING CORNEFORM BACTERIA  
FILE REFERENCE: 21123/282414/MAS  
CURRENT APPLICATION NUMBER: US/09/951,536  
CURRENT FILING DATE: 2001-09-14  
PRIOR APPLICATION NUMBER: 09/431,099  
PRIOR FILING DATE: 1999-11-01  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 489  
TYPE: PRN  
ORGANISM: Corynebacterium glutamicum  
US-09-951-536-4

Query Match 100.0%; Score 2432; DB 9; Length 489;  
Best Local Similarity 100.0%; Pred. No. 4.5e-214;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 481 TNORFNGKR 489  
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RESULT 3  
US-09-963-521-2  
Sequence 2, Application US/09963521  
Patent No. US20020146781A1  
GENERAL INFORMATION:  
APPLICANT: ZIEGLER, PETRA  
APPLICANT: EGGELING, LOTMAR  
APPLICANT: SAHM, HERMANN  
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE  
TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF  
TITLE OF INVENTION: L-THREONINE USING CORNEFORM BACTERIA  
FILE REFERENCE: 21123/282413/MAS  
CURRENT APPLICATION NUMBER: US/09/963,521  
CURRENT FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: 09/431,099  
PRIOR FILING DATE: 1999-11-01  
PRIOR APPLICATION NUMBER: DE 199 41 478.5  
PRIOR FILING DATE: 1999-09-01  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 489  
TYPE: PRN  
ORGANISM: Corynebacterium glutamicum  
US-09-963-521-2

Query Match 100.0%; Score 2432; DB 9; Length 489;  
Best Local Similarity 100.0%; Pred. No. 4.5e-214;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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US-09-963-521-4  
; Sequence 4, Application US/09963521  
; Patent No. US20020146781A1  
; GENERAL INFORMATION:  
; APPLICANT: ZIEGLER, PETRA  
; APPLICANT: EGGELING, LOTMAR  
; APPLICANT: SAHM, HERMANN  
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE  
; TITLE OF INVENTION: AND PROCESS FOR THE ENZYMAIC PRODUCTION OF  
; TITLE OF INVENTION: L-THREONINE USING CORINEFORM BACTERIA  
; FILE REFERENCE: 21123/282413/MAS  
; CURRENT APPLICATION NUMBER: US/09/963,521  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: 09/431,099  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: DE 199 41 478.5  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 489  
; TYPE: PRF  
; ORGANISM: Corynebacterium glutamicum  
US-09-963-521-4

Query Match 100.0%; Score 2432; DB 9; Length 489;  
Best Local Similarity 100.0%; Pred. No. 4.5e-214;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 421 AVALATASSLAAGVVLGEMTARRLRPPRPYRAFTKANESFOEAEONORORRKP 480  
Qy 481 TNORFGNKR 489  
Db 481 TNORFGNKR 489

## RESULT 5

US-09-834-721-2  
; Sequence 2, Application US/09834721  
; Patent No. US2002015551A1  
; GENERAL INFORMATION:  
; APPLICANT: RIEPING, MECHTILD  
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE  
; FILE REFERENCE: 21123/280169/MAS  
; CURRENT APPLICATION NUMBER: US/09/834,721  
; PRIOR FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: DE 100 26 494.8  
; PRIOR FILING DATE: 2000-05-27  
; PRIOR APPLICATION NUMBER: DE 101 02 823.7  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 489  
; TYPE: PRF  
; ORGANISM: Corynebacterium glutamicum  
; FEATURE:  
; OTHER INFORMATION: ATCC14752  
US-09-834-721-2

Query Match 100.0%; Score 2432; DB 9; Length 489;  
Best Local Similarity 100.0%; Pred. No. 4.5e-214;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 481 TNORFGNKR 489

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RESULT 6
US-09-834-721-4
; Sequence 4, Application US/09834721
; Patent No. US20020155551A1
; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTHILD
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
; FILE REFERENCE: 21123/280169/MAS
; CURRENT APPLICATION NUMBER: US/09/834,721
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: DE 100 26 494.8
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: DE 101 02 823.7
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 489
; TYPE: PRF
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: ATCC13032
US-09-834-721-4

Query Match      100.0%; Score 2432; DB 9; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.5e-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MTSFATLRGISTVDAAKAPPSPLAPIDLTDSQVAGVNNLAARIGDILLSSGTSNSD 60
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DB 121 RLIRSIQAGATPPEVAEKILDELEQSPASVGFPAALLGMAMGGAVALVLLGGQVSLIA 180
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DB 481 TNORFGNKR 489

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APPLICANT: Sahn, Hermann
APPLICANT: Thierbach, Georg
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
TITLE OF INVENTION: PROCESS FOR
TITLE OF INVENTION: ENZYMAIC PRODUCTION OF L-THREONINE USING CORYNEFORM BACTERIA
FILE REFERENCE: 21123/277066
CURRENT APPLICATION NUMBER: US/09/783,388
CURRENT FILING DATE: 2001-02-15
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 489
TYPE: PRF
ORGANISM: Corynebacterium glutamicum ATCC14752
US-09-783-388-2

Query Match      100.0%; Score 2432; DB 9; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.5e-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSFATLRGISTVDAAKAPPSPLAPIDLTDSQVAGVNNLAARIGDILLSSGTSNSD 60
DB 1 MTSFATLRGISTVDAAKAPPSPLAPIDLTDSQVAGVNNLAARIGDILLSSGTSNSD 60
QY 61 TKQVRAVTSAGLYYTHVDITNTITITFTNIGVERKMPVNVFHVVGKLDTNFSKLEVD 120
DB 61 TKQVRAVTSAGLYYTHVDITNTITITFTNIGVERKMPVNVFHVVGKLDTNFSKLEVD 120
QY 121 RLIRSIQAGATPPEVAEKILDELEQSPASVGFPAALLGMAMGGAVALVLLGGQVSLIA 180
DB 121 RLIRSIQAGATPPEVAEKILDELEQSPASVGFPAALLGMAMGGAVALVLLGGQVSLIA 180
QY 121 RLIRSIQAGATPPEVAEKILDELEQSPASVGFPAALLGMAMGGAVALVLLGGQVSLIA 180
DB 121 RLIRSIQAGATPPEVAEKILDELEQSPASVGFPAALLGMAMGGAVALVLLGGQVSLIA 180
QY 181 FITAFITLITTSFSGKGLPTFPONVVGFTATLPASIAVSIALQFGLIKPSQIIASGI 240
DB 181 FITAFITLITTSFSGKGLPTFPONVVGFTATLPASIAVSIALQFGLIKPSQIIASGI 240
QY 241 VVLAGLTLVQSLQDGTGATGAVTASARFFETLLFTGIVAGVGIGIQLSEILHVMLEPAME 300
DB 241 VVLAGLTLVQSLQDGTGATGAVTASARFFETLLFTGIVAGVGIGIQLSEILHVMLEPAME 300
QY 301 SAAAPNYSSTFARIIAGVTAAPAVGCVYAEWSSVITAGTALMGSAFYVLFVYVLLGVS 360
DB 301 SAAAPNYSSTFARIIAGVTAAPAVGCVYAEWSSVITAGTALMGSAFYVLFVYVLLGVS 360
QY 301 SAAAPNYSSTFARIIAGVTAAPAVGCVYAEWSSVITAGTALMGSAFYVLFVYVLLGVS 360
DB 301 SAAAPNYSSTFARIIAGVTAAPAVGCVYAEWSSVITAGTALMGSAFYVLFVYVLLGVS 360
QY 361 AAATAATVGTGGLARRFLIPLIYVAGITPMLPGALYRGMVATLNDQTLMGFTNI 420
DB 361 AAATAATVGTGGLARRFLIPLIYVAGITPMLPGALYRGMVATLNDQTLMGFTNI 420
QY 421 AVALATASSLAGVVLGEMIAARRLRPPRFNPYRAFTKANESFOEAEONQRRKRPK 480
DB 421 AVALATASSLAGVVLGEMIAARRLRPPRFNPYRAFTKANESFOEAEONQRRKRPK 480
QY 481 TNORFGNKR 489
DB 481 TNORFGNKR 489

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RESULT 7
US-09-783-388-2
; Sequence 2, Application US/09783388
; Patent No. US20020168731A1
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Petra
; APPLICANT: Eggeling, Lothar
; APPLICANT: Sahn, Hermann
; APPLICANT: Thierbach, Georg
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
TITLE OF INVENTION: PROCESS FOR
TITLE OF INVENTION: ENZYMAIC PRODUCTION OF L-THREONINE USING CORYNEFORM BACTERIA
FILE REFERENCE: 21123/277066
CURRENT APPLICATION NUMBER: US/09/783,388
CURRENT FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 8

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum ATCC13032
US-09-783-388-4

Query Match      100.0%; Score 2432; DB 9; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.5e-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSFATLRGRISTVDAAKAAAPPSPLAPIDLTDHSQVAGVWNLAAIRIGDILLSSGTSNSD 60
DB 1 MLSFATLRGRISTVDAAKAAAPPSPLAPIDLTDHSQVAGVWNLAAIRIGDILLSSGTSNSD 60
QY 61 TKQVRAVTSAYGLYTHVDITLNTTITFTNIGVERMPVNVHVVKLDTNFSKLSVD 120
DB 61 TKQVRAVTSAYGLYTHVDITLNTTITFTNIGVERMPVNVHVVKLDTNFSKLSVD 120
QY 121 RLIRSIQAGATPPEVAKIIDELEQSPASYGFVALLGMAMGGAVAVLLGGGQVSLIA 180
DB 121 RLIRSIQAGATPPEVAKIIDELEQSPASYGFVALLGMAMGGAVAVLLGGGQVSLIA 180
QY 121 RLIRSIQAGATPPEVAKIIDELEQSPASYGFVALLGMAMGGAVAVLLGGGQVSLIA 180
DB 121 RLIRSIQAGATPPEVAKIIDELEQSPASYGFVALLGMAMGGAVAVLLGGGQVSLIA 180
QY 181 FITAFTIIATTSFLGKKGLPTFFQNVVGFIALTPASIAVSLALQFGLERKPSQIIASGI 240
DB 181 FITAFTIIATTSFLGKKGLPTFFQNVVGFIALTPASIAVSLALQFGLERKPSQIIASGI 240
QY 241 VLLAGLITVQSIQDGGITGAPVTASARFFETLLFTGGIVAGVGLIQLSILLHVMLEPAME 300
DB 241 VLLAGLITVQSIQDGGITGAPVTASARFFETLLFTGGIVAGVGLIQLSILLHVMLEPAME 300
QY 301 SAAAPNVSTFARIIAGGVTAAPAVGCVAEWSSVIIAGLTALMGSAFYLLFVYVLGPVS 360
DB 301 SAAAPNVSTFARIIAGGVTAAPAVGCVAEWSSVIIAGLTALMGSAFYLLFVYVLGPVS 360
QY 361 AAAIAATAVGFOTGLLARRELPPLIYALIGITPMLPGALYRGMTATLNDQTLMGFTNI 420
DB 361 AAAIAATAVGFOTGLLARRELPPLIYALIGITPMLPGALYRGMTATLNDQTLMGFTNI 420
QY 421 AVALATASSLAAGVVGEMTARLRPRPNPYRAFTKANEFSFOEAEONORQRPRK 480
DB 421 AVALATASSLAAGVVGEMTARLRPRPNPYRAFTKANEFSFOEAEONORQRPRK 480
QY 481 TNORFGNKR 489
DB 481 TNORFGNKR 489

RESULT 9
US-09-951-535-2
; Sequence 2, Application US/09951535
; Publication No. US20030049802A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELENG, LOTMAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
; FILE REFERENCE: 21123/282415/MAS
; CURRENT APPLICATION NUMBER: US/09/951,535
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478.5
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
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US-09-951-535-2

Query Match      100.0%; Score 2432; DB 10; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.5e-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSFATLRGRISTVDAAKAAAPPSPLAPIDLTDHSQVAGVWNLAAIRIGDILLSSGTSNSD 60
DB 1 MLSFATLRGRISTVDAAKAAAPPSPLAPIDLTDHSQVAGVWNLAAIRIGDILLSSGTSNSD 60
QY 61 TKQVRAVTSAYGLYTHVDITLNTTITFTNIGVERMPVNVHVVKLDTNFSKLSVD 120
DB 61 TKQVRAVTSAYGLYTHVDITLNTTITFTNIGVERMPVNVHVVKLDTNFSKLSVD 120
QY 121 RLIRSIQAGATPPEVAKIIDELEQSPASYGFVALLGMAMGGAVAVLLGGGQVSLIA 180
DB 121 RLIRSIQAGATPPEVAKIIDELEQSPASYGFVALLGMAMGGAVAVLLGGGQVSLIA 180
QY 181 FITAFTIIATTSFLGKKGLPTFFQNVVGFIALTPASIAVSLALQFGLERKPSQIIASGI 240
DB 181 FITAFTIIATTSFLGKKGLPTFFQNVVGFIALTPASIAVSLALQFGLERKPSQIIASGI 240
QY 241 VLLAGLITVQSIQDGGITGAPVTASARFFETLLFTGGIVAGVGLIQLSILLHVMLEPAME 300
DB 241 VLLAGLITVQSIQDGGITGAPVTASARFFETLLFTGGIVAGVGLIQLSILLHVMLEPAME 300
QY 301 SAAAPNVSTFARIIAGGVTAAPAVGCVAEWSSVIIAGLTALMGSAFYLLFVYVLGPVS 360
DB 301 SAAAPNVSTFARIIAGGVTAAPAVGCVAEWSSVIIAGLTALMGSAFYLLFVYVLGPVS 360
QY 361 AAAIAATAVGFOTGLLARRELPPLIYALIGITPMLPGALYRGMTATLNDQTLMGFTNI 420
DB 361 AAAIAATAVGFOTGLLARRELPPLIYALIGITPMLPGALYRGMTATLNDQTLMGFTNI 420
QY 421 AVALATASSLAAGVVGEMTARLRPRPNPYRAFTKANEFSFOEAEONORQRPRK 480
DB 421 AVALATASSLAAGVVGEMTARLRPRPNPYRAFTKANEFSFOEAEONORQRPRK 480
QY 481 TNORFGNKR 489
DB 481 TNORFGNKR 489

RESULT 10
US-09-951-535-4
; Sequence 4, Application US/09951535
; Publication No. US20030049802A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELENG, LOTMAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
; FILE REFERENCE: 21123/282415/MAS
; CURRENT APPLICATION NUMBER: US/09/951,535
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478.5
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-951-535-4

Query Match      100.0%; Score 2432; DB 10; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.5e-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MLSPATLRGRISTVDAAKAAAPPSPPLAPIDLTDSQVAGVNNLAARIGDILLSSGTSNSD 60
DB 1 MLSPATLRGRISTVDAAKAAAPPSPPLAPIDLTDSQVAGVNNLAARIGDILLSSGTSNSD 60
QY 61 TKQVRAVTSAYGGLYTHVDITLNTITITFTNIGVERKMPVVFHVVGKLDITNFSKLSVD 120
DB 61 TKQVRAVTSAYGGLYTHVDITLNTITITFTNIGVERKMPVVFHVVGKLDITNFSKLSVD 120
QY 121 RLRSIQAGATPPEVAEKIDLEQSPASVGFVALLGMAMGGAVALLGGMQVSLIA 180
DB 121 RLRSIQAGATPPEVAEKIDLEQSPASVGFVALLGMAMGGAVALLGGMQVSLIA 180
QY 181 FITFTIATTSFEGKGLPFFQNVVGGFTATLPASIAVSIALQFGLEIKPSQIIASGI 240
DB 181 FITFTIATTSFEGKGLPFFQNVVGGFTATLPASIAVSIALQFGLEIKPSQIIASGI 240
QY 241 VVLAGLTLVOSLDGDTGAPVTASARFFETLLFTGGIVAGVGIGIOSEILHVMPLAME 300
DB 241 VVLAGLTLVOSLDGDTGAPVTASARFFETLLFTGGIVAGVGIGIOSEILHVMPLAME 300
QY 301 SAAAPNVSSTFARIIAGVTAAPAVGCVYAEWSSVIIAGLTALMGSAFYLLFVYVLGPVS 360
DB 301 SAAAPNVSSTFARIIAGVTAAPAVGCVYAEWSSVIIAGLTALMGSAFYLLFVYVLGPVS 360
QY 361 AAAATAATVGTGGILARRFLIPLIYVAGITPMLPGLAIYRGMVATLNDQTLMGFTNI 420
DB 361 AAAATAATVGTGGILARRFLIPLIYVAGITPMLPGLAIYRGMVATLNDQTLMGFTNI 420
QY 421 AVALATASSLAGVVLGEMWIRLRPRFPNYPYRAFTKANEFSFOEAEQORQRKPK 480
DB 421 AVALATASSLAGVVLGEMWIRLRPRFPNYPYRAFTKANEFSFOEAEQORQRKPK 480
QY 481 TNORFGNKR 489
DB 481 TNORFGNKR 489

RESULT 11
US-10-627-476-558
; Sequence 558, Application US/10627476
; Publication No. US20040030116A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Mark
; APPLICANT: Krieger, Burkhard
; APPLICANT: Schoder, Hartwig
; APPLICANT: Zeider, Oskar
; APPLICANT: Haberer, Gregor
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CPN
; CURRENT APPLICATION NUMBER: US/10/627.476
; PUBLICATION DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 09/602,787
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
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;; PRIOR FILING DATE: 1999-07-09
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 678
;; SEQ ID NO 558
;; LENGTH: 489
;; TYPE: PRT
;; ORGANISM: Corynebacterium glutamicum
US-10-627-476-558

Query Match 100.0%; Score 2432; DB 12; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.5e-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSPATLRGRISTVDAAKAAAPPSPPLAPIDLTDSQVAGVNNLAARIGDILLSSGTSNSD 60
DB 1 MLSPATLRGRISTVDAAKAAAPPSPPLAPIDLTDSQVAGVNNLAARIGDILLSSGTSNSD 60
QY 61 TKQVRAVTSAYGGLYTHVDITLNTITITFTNIGVERKMPVVFHVVGKLDITNFSKLSVD 120
DB 61 TKQVRAVTSAYGGLYTHVDITLNTITITFTNIGVERKMPVVFHVVGKLDITNFSKLSVD 120
QY 121 RLRSIQAGATPPEVAEKIDLEQSPASVGFVALLGMAMGGAVALLGGMQVSLIA 180
DB 121 RLRSIQAGATPPEVAEKIDLEQSPASVGFVALLGMAMGGAVALLGGMQVSLIA 180
QY 181 FITFTIATTSFEGKGLPFFQNVVGGFTATLPASIAVSIALQFGLEIKPSQIIASGI 240
DB 181 FITFTIATTSFEGKGLPFFQNVVGGFTATLPASIAVSIALQFGLEIKPSQIIASGI 240
QY 241 VVLAGLTLVOSLDGDTGAPVTASARFFETLLFTGGIVAGVGIGIOSEILHVMPLAME 300
DB 241 VVLAGLTLVOSLDGDTGAPVTASARFFETLLFTGGIVAGVGIGIOSEILHVMPLAME 300
QY 301 SAAAPNVSSTFARIIAGVTAAPAVGCVYAEWSSVIIAGLTALMGSAFYLLFVYVLGPVS 360
DB 301 SAAAPNVSSTFARIIAGVTAAPAVGCVYAEWSSVIIAGLTALMGSAFYLLFVYVLGPVS 360
QY 361 AAAATAATVGTGGILARRFLIPLIYVAGITPMLPGLAIYRGMVATLNDQTLMGFTNI 420
DB 361 AAAATAATVGTGGILARRFLIPLIYVAGITPMLPGLAIYRGMVATLNDQTLMGFTNI 420
QY 421 AVALATASSLAGVVLGEMWIRLRPRFPNYPYRAFTKANEFSFOEAEQORQRKPK 480
DB 421 AVALATASSLAGVVLGEMWIRLRPRFPNYPYRAFTKANEFSFOEAEQORQRKPK 480
QY 481 TNORFGNKR 489
DB 481 TNORFGNKR 489

RESULT 12
US-10-450-055-42
; Sequence 42, Application US/10450055
; Publication No. US20040043953A1
; GENERAL INFORMATION:
; APPLICANT: BASF Aktiengesellschaft
; TITLE OF INVENTION: No. US20040043953A1 genes of Corynebacterium
; FILE REFERENCE: 936 2000
; CURRENT APPLICATION NUMBER: US/10/450.055
; PUBLICATION DATE: 2003-06-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 42
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-450-055-42

Query Match 100.0%; Score 2432; DB 12; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.5e-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSPATLRGRISTVDAAKAAAPPSPPLAPIDLTDSQVAGVNNLAARIGDILLSSGTSNSD 60
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Db 1 MLSPATLRGRISTVDAAKAAAPPSPPLAPIDLTDHSGVAGVNMNLAARIGDILLSSGTSNSD 60  
QY 61 TKVQRAVTSAYGLYYTHVDITLNTITITFTNIGVERKMPVNVFHVVGKLDITNFSKLSVD 120  
Db 61 TKVQRAVTSAYGLYYTHVDITLNTITITFTNIGVERKMPVNVFHVVGKLDITNFSKLSVD 120  
QY 121 RLIRSIQAGATPEPVAEKLIDELQSPASYSYGPVALLGMAWGGAAVAVLLGGGWQVSLIA 180  
Db 121 RLIRSIQAGATPEPVAEKLIDELQSPASYSYGPVALLGMAWGGAAVAVLLGGGWQVSLIA 180  
QY 181 FITAFITIAATTSFLGKKGLPTFFQNVVGGFIATLPASIAVSLALQFGLTKPSQIIASGI 240  
Db 181 FITAFITIAATTSFLGKKGLPTFFQNVVGGFIATLPASIAVSLALQFGLTKPSQIIASGI 240  
QY 241 VVLAGLTLVOSLQDGIITGAPVTASARFETLLFTGGIIVAGVGIGIQSEILHVMLEPAME 300  
Db 241 VVLAGLTLVOSLQDGIITGAPVTASARFETLLFTGGIIVAGVGIGIQSEILHVMLEPAME 300  
QY 301 SAAAPNYSSTFARIIAGVTAFAVAVGCVAMSSVITAGLTALMGSAFYVLFVYVLGPVS 360  
Db 301 SAAAPNYSSTFARIIAGVTAFAVAVGCVAMSSVITAGLTALMGSAFYVLFVYVLGPVS 360  
QY 361 AAAAATAVGTGGLARRFLIPLIYAIGITPMLPGAIYRGMYATINDQTLMGFTNI 420  
Db 361 AAAAATAVGTGGLARRFLIPLIYAIGITPMLPGAIYRGMYATINDQTLMGFTNI 420  
QY 421 AVAATATSSIAAGVTLGEMTARLRIRDPRENPYAFATKANEFSFOEBAEQNRQRKRPX 480  
Db 421 AVAATATSSIAAGVTLGEMTARLRIRDPRENPYAFATKANEFSFOEBAEQNRQRKRPX 480  
QY 481 TNORFGNKR 489  
Db 481 TNORFGNKR 489

RESULT 13  
US-10-224-574-10  
; Sequence 10, Application US/10224574  
; Publication No. US20040101837A1  
; GENERAL INFORMATION:  
; APPLICANT: Forschungszentrum Jlich GmbH; P. Ziegler, L. Eggeling, H. Sahm,  
; APPLICANT: P. Peters- Wendisch  
; TITLE OF INVENTION: Nucleotide sequences coding for proteins participating in the syt  
; TITLE OF INVENTION: L-serin, improved process for the microbial manufacture of L-ser  
; TITLE OF INVENTION: genetically modified microorganism suitable for the process.  
; FILE REFERENCE: FZJ-9912-PCT  
; CURRENT APPLICATION NUMBER: US/10/224,574  
; CURRENT FILING DATE: 2002-08-21  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 489  
; TYPE: PRT  
; ORGANISM: C. glutamicum ATCC 14 752  
US-10-224-574-10

Query Match 100.0%; Score 2432; DB 16; Length 489;  
Best Local Similarity 100.0%; Pred. No. 4.5e-214;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSFATLRGRISTVDAAKAAAPPSPPLAPIDLTDHSGVAGVNMNLAARIGDILLSSGTSNSD 60  
Db 1 MLSFATLRGRISTVDAAKAAAPPSPPLAPIDLTDHSGVAGVNMNLAARIGDILLSSGTSNSD 60  
QY 61 TKVQRAVTSAYGLYYTHVDITLNTITITFTNIGVERKMPVNVFHVVGKLDITNFSKLSVD 120  
Db 61 TKVQRAVTSAYGLYYTHVDITLNTITITFTNIGVERKMPVNVFHVVGKLDITNFSKLSVD 120  
QY 121 RLIRSIQAGATPEPVAEKLIDELQSPASYSYGPVALLGMAWGGAAVAVLLGGGWQVSLIA 180  
Db 121 RLIRSIQAGATPEPVAEKLIDELQSPASYSYGPVALLGMAWGGAAVAVLLGGGWQVSLIA 180

QY 181 FITAFITIAATTSFLGKKGLPTFFQNVVGGFIATLPASIAVSLALQFGLTKPSQIIASGI 240  
Db 181 FITAFITIAATTSFLGKKGLPTFFQNVVGGFIATLPASIAVSLALQFGLTKPSQIIASGI 240  
QY 241 VVLAGLTLVOSLQDGIITGAPVTASARFETLLFTGGIIVAGVGIGIQSEILHVMLEPAME 300  
Db 241 VVLAGLTLVOSLQDGIITGAPVTASARFETLLFTGGIIVAGVGIGIQSEILHVMLEPAME 300  
QY 301 SAAAPNYSSTFARIIAGVTAFAVAVGCVAMSSVITAGLTALMGSAFYVLFVYVLGPVS 360  
Db 301 SAAAPNYSSTFARIIAGVTAFAVAVGCVAMSSVITAGLTALMGSAFYVLFVYVLGPVS 360  
QY 361 AAAAATAVGTGGLARRFLIPLIYAIGITPMLPGAIYRGMYATINDQTLMGFTNI 420  
Db 361 AAAAATAVGTGGLARRFLIPLIYAIGITPMLPGAIYRGMYATINDQTLMGFTNI 420  
QY 421 AVAATATSSIAAGVTLGEMTARLRIRDPRENPYAFATKANEFSFOEBAEQNRQRKRPX 480  
Db 421 AVAATATSSIAAGVTLGEMTARLRIRDPRENPYAFATKANEFSFOEBAEQNRQRKRPX 480  
QY 481 TNORFGNKR 489  
Db 481 TNORFGNKR 489

RESULT 14  
US-10-224-574-12  
; Sequence 12, Application US/10224574  
; Publication No. US20040101837A1  
; GENERAL INFORMATION:  
; APPLICANT: Forschungszentrum Jlich GmbH; P. Ziegler, L. Eggeling, H. Sahm,  
; APPLICANT: P. Peters- Wendisch  
; TITLE OF INVENTION: Nucleotide sequences coding for proteins participating in the syt  
; TITLE OF INVENTION: L-serin, improved process for the microbial manufacture of L-ser  
; TITLE OF INVENTION: genetically modified microorganism suitable for the process.  
; FILE REFERENCE: FZJ-9912-PCT  
; CURRENT APPLICATION NUMBER: US/10/224,574  
; CURRENT FILING DATE: 2002-08-21  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 489  
; TYPE: PRT  
; ORGANISM: C. glutamicum ATCC 13 032  
US-10-224-574-12

Query Match 100.0%; Score 2432; DB 16; Length 489;  
Best Local Similarity 100.0%; Pred. No. 4.5e-214;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSFATLRGRISTVDAAKAAAPPSPPLAPIDLTDHSGVAGVNMNLAARIGDILLSSGTSNSD 60  
Db 1 MLSFATLRGRISTVDAAKAAAPPSPPLAPIDLTDHSGVAGVNMNLAARIGDILLSSGTSNSD 60  
QY 61 TKVQRAVTSAYGLYYTHVDITLNTITITFTNIGVERKMPVNVFHVVGKLDITNFSKLSVD 120  
Db 61 TKVQRAVTSAYGLYYTHVDITLNTITITFTNIGVERKMPVNVFHVVGKLDITNFSKLSVD 120  
QY 121 RLIRSIQAGATPEPVAEKLIDELQSPASYSYGPVALLGMAWGGAAVAVLLGGGWQVSLIA 180  
Db 121 RLIRSIQAGATPEPVAEKLIDELQSPASYSYGPVALLGMAWGGAAVAVLLGGGWQVSLIA 180  
QY 181 FITAFITIAATTSFLGKKGLPTFFQNVVGGFIATLPASIAVSLALQFGLTKPSQIIASGI 240  
Db 181 FITAFITIAATTSFLGKKGLPTFFQNVVGGFIATLPASIAVSLALQFGLTKPSQIIASGI 240  
QY 241 VVLAGLTLVOSLQDGIITGAPVTASARFETLLFTGGIIVAGVGIGIQSEILHVMLEPAME 300  
Db 241 VVLAGLTLVOSLQDGIITGAPVTASARFETLLFTGGIIVAGVGIGIQSEILHVMLEPAME 300  
QY 301 SAAAPNYSSTFARIIAGVTAFAVAVGCVAMSSVITAGLTALMGSAFYVLFVYVLGPVS 360  
Db 301 SAAAPNYSSTFARIIAGVTAFAVAVGCVAMSSVITAGLTALMGSAFYVLFVYVLGPVS 360

QY 361 AAAIATAVGFTGGLARRFLIPPLIVAIAGITPMLPGAIYRGWYATINDOTLMGFTNI 420  
 DB 361 AAAIATAVGFTGGLARRFLIPPLIVAIAGITPMLPGAIYRGWYATINDOTLMGFTNI 420  
 QY 421 AVALATASSIAAGVIGEWIARLRPRPNPYRAFTKNEFSFOEAEQNRORRKP 480  
 DB 421 AVALATASSIAAGVIGEWIARLRPRPNPYRAFTKNEFSFOEAEQNRORRKP 480  
 QY 481 TNORFGNKR 489  
 DB 481 TNORFGNKR 489

RESULT 15

US-09-738-626-6384  
 ; Sequence 6384, Application US/09738626  
 ; Publication No. US20020197605A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NAKAGAWA, SATOSHI  
 ; APPLICANT: MIZOGUCHI, HIROSHI  
 ; APPLICANT: ANDO, SEIKO  
 ; APPLICANT: HAYASHI, MIKIRO  
 ; APPLICANT: OCHIAI, KEIKO  
 ; APPLICANT: YOKOI, HARUHIKO  
 ; APPLICANT: TATEISHI, NAOKO  
 ; APPLICANT: SENOH, AKIHIRO  
 ; APPLICANT: IKEDA, MASATO  
 ; APPLICANT: OZAKI, AKIO  
 ; TITLE OR INVENTION: NOVEL POLYNUCLEOTIDES  
 ; FILE REFERENCE: 249-125  
 ; CURRENT APPLICATION NUMBER: US/09/738, 626  
 ; CURRENT FILING DATE: 2000-12-18  
 ; PRIOR APPLICATION NUMBER: JP 99/377484  
 ; PRIOR FILING DATE: 1999-12-16  
 ; PRIOR APPLICATION NUMBER: JP 00/159162  
 ; PRIOR FILING DATE: 2000-04-07  
 ; PRIOR APPLICATION NUMBER: JP 00/280988  
 ; PRIOR FILING DATE: 2000-08-03  
 ; NUMBER OF SEQ ID NOS: 7059  
 ; SOFTWARE: PatentIn ver. 3.0  
 ; SEQ ID NO 6384  
 ; LENGTH: 501  
 ; TYPE: PRT  
 ; ORGANISM: Corynebacterium glutamicum  
 US-09-738-626-6384

Query Match 100.0%; Score 2432; DB 9; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-214;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MISFATLGRISTVDAAKAPPPSLAPIDLTDHSQVAGVMMLAARIGDILISGTSNSD 60  
 DB 13 MISFATLGRISTVDAAKAPPPSLAPIDLTDHSQVAGVMMLAARIGDILISGTSNSD 72  
 QY 61 TKQVRAVTSAYGLYTHVDITLNTITFTNIGVERKMPVNFHVVGKLDINFSKLSVD 120  
 DB 73 TKQVRAVTSAYGLYTHVDITLNTITFTNIGVERKMPVNFHVVGKLDINFSKLSVD 132  
 QY 121 RLIRSIQAGATPEVAEKILDELQSPASGYGFVALIGWAMMGAVAVLLGGWQVSLIA 180  
 DB 121 RLIRSIQAGATPEVAEKILDELQSPASGYGFVALIGWAMMGAVAVLLGGWQVSLIA 192  
 QY 181 FITAFITIAATSTFLGKGLPTFFONVVGFIATLPASIAVSLALQGLEIKPSQIIASGI 240  
 DB 181 FITAFITIAATSTFLGKGLPTFFONVVGFIATLPASIAVSLALQGLEIKPSQIIASGI 252  
 QY 241 VVLLAGLTIVOSIQCITGAPVTASARFETILLFTGCIYAGVGLGIQISEIILHVMIPAME 300  
 DB 241 VVLLAGLTIVOSIQCITGAPVTASARFETILLFTGCIYAGVGLGIQISEIILHVMIPAME 312  
 QY 301 SAAAPNYSSTFARIINGVTAFAAFAVGCAEWSVLIAGLTALMSGAFYLLFVVYLG PVS 360

DB 313 SAAAPNYSSTFARIINGVTAFAAFAVGCAEWSVLIAGLTALMSGAFYLLFVVYLG PVS 372  
 QY 361 AAAIATAVGFTGGLARRFLIPPLIVAIAGITPMLPGAIYRGWYATINDOTLMGFTNI 420  
 DB 373 AAAIATAVGFTGGLARRFLIPPLIVAIAGITPMLPGAIYRGWYATINDOTLMGFTNI 432  
 QY 421 AVALATASSIAAGVIGEWIARLRPRPNPYRAFTKNEFSFOEAEQNRORRKP 480  
 DB 421 AVALATASSIAAGVIGEWIARLRPRPNPYRAFTKNEFSFOEAEQNRORRKP 492  
 QY 481 TNORFGNKR 489  
 DB 481 TNORFGNKR 501

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 Job time : 1070 secs